1 CCGCAACCCC GACGGCGCCC CAAACGCTGT TGCGCCGCGC GCCCCGCCCA
51 GCCCGGCCTC GCGCTGGTCC CGGTCTCGCC CCGCAGCCCT CGATCTCCCG
101 TGACTTCCTC GGCCAGGCCG CCTGCGCCTC TGGGACCATG TTGCGCTGGC
151 TGCGGGACTT CGCGCTGCCC ACCGCGGCCT GCCAGGACGC GGAGCAGCCG
201 ACGCGCTACG AGACCCTCTT CCAGGCACTG GACCGCAATG GGGACGGAGT
251 GGTGGACATC GGCGAGCTGC AGGAGGGGCT CAGGAACCTG GGCATCCCTC
301 TGGGCCAGGA CGCCGAGGAG AAAATTTTTA CTACTGGAGA TGTCAACAAA
351 GATGGGAAGC TGGATTTTGA AGAATTTATG AAGTACCTTA AAGACCATGA
401 GAAGAAAATG AAATTGGCAT TTAAGAGTTT AGACAAAAAT AATGATGGAA
451 AAATTGAGGC TTCAGAAATT GTCCAGTCTC TCCAGACACT GGGTCTGACT
501 ATTTCTGAAC AACAAGCAGA GTTGATTCTT CAAAGCATTG ATGTTGATGG
551 GACAATGACA GTGGACTGGA ATGAATGGAG AGACTACTTC TTATTTAATC
601 CTGTTACAGA CATTGAGGAA ATTATCCGTT TCTGGAAACA TTCTACAGGA
651 ATTGACATAG GGGATAGCTT AACTATTCCA GATGAATTCA CGGAAGACGA
701 AAAAAAATCC GGACAATGGT GGAGGCAGCT TTTGGCAGGA GGCATTGCTG
751 GTGCTGTCTC TCGAACAAGC ACTGCCCCTT TGGACCGTCT GAAAATCATG
801 ATGCAGGTTC ACGGTTCAAA ATCAGACAAA ATGAACATAT TTGGTGGCTT
851 TCGACAGATG GTAAAAGAAG GAGGTATCCG CTCGCTTTGG AGGGGAAATG
901 GTACAAACGT CATCAAAATT GCTCCTGAGA CAGCTGTTAA ATTCTGGGCA
951 TATGAACAGT ACAAGAAGTT ACTTACTGAA GAAGGACAAA AAATAGGAAC
1001 ATTTGAGAGA TTTATTTCTG GTTCCATGGC TGGAGCAACT GCACAGACTT
1051 TTATATATCC AATGGAGGTT ATGAAAACCA GGCTGGCTGT AGGCAAAACT
1101 GGGCAGTACT CTGGAATATA TGATTGTGCC AAGAAGATTT TGAAACATGA
1151 AGGCTTGGGA GCTTTTTACA AAGGCTATGT TCCCAATTTA TTAGGTATCA
1201 TACCTTATGC AGGCATAGAT CTTGCTGTGT ATGAGCTCTT GAAGTCCTAT
1251 TGGCTGGATA ATTTTGCAAA AGATTCTGTA AACCCTGGAG TCATGGTGTT
1301 GCTGGGATGC GGTGCCTTAT CCAGCACCTG TGGTCAGCTG GCCAGCTACC
1351 CATTGGCTTT GGTGAGAACT CGCATGCAGG CTCAAGCCAT GTTAGAAGGT
1401 TCCCCACAGC TGAATATGGT TGGCCTCTTT CGACGAATTA TTTCCAAAGA
1451 AGGAATACCA GGACTTTACA GAGGCATCAC CCCAAACTTC ATGAAGGTGC
1501 TCCCTGCTGT AGGCATCAGT TATGTGGTTT ATGAAAATAT GAAGCAAACT
1551 TTAGGAGTAA CCCAGAAATG ATGTTGCATT TTTTGCTTTA GCCTGATAAT
1601 TGAAACTTTC AACAATCTCT GGAGTGACTT TTTCTCCTCG AATTGAAACA
1651 AGTCTATGGC AAAAGAAGCT GCATTTTTTT CACAAAAGGG AAGACGGTAA
1701 CAATGGTCAC TTCAAACTTT TGGGCTAAAT TATATGTACA CAGAAATGTT
1751 CAAAATCATA GTTTTAATGT GTTTTGAAAA GGCCACACAA TTATACTTTA
1801 TCTTTTCTTA ATAATCCTGC AAATCTCTGC CCTGAATCCG AAATCTGAAA
1851 ATGTACTGGC TTGAACAAAA TTTGTTTTGT GTGTTAGAGT TATAAATCAT
1901 TAATCTTTAT TTCGGGTGGT TTACGTTTAT GCCAGTTCCT TTATATTTAA
1951 ATTTCTTGTT TTATATATTT TGAATGTCTT TATAGATTTC TTTAAATTTC
2001 CTTATAGAAC CATTAATAGA AAATCATTAC ATTTAAAATA TACCTTACAG
2051 CAAAAGCATC CAAATAAGTA TAGGGTTTAT GTCCTTATTT TTCTTTCAGC
2101 TGAATACGAA TGAACACAGT GGTGGAATTT CTGAAGGGAA GTGATGAAAT
2151 TATATTTATT TCAGTGGGCA CTTTTCCATT TTACCACTGT ACCATTATTT
2201 GGTTCCTGGA GTTATACACT AATTTTCAGT ATATTACTGT TAAATTACCA
2251 ACACAAGGCA ATTTATTTGA AAGATTCCGT TTATCCTGCC ATTGCTTTGA
2301 AAAGCAGCAG GAAACGAAAT TTTTTGACTT GTATCAGCTT CTGCAGAGCA
2351 TCTTTGTTTT CCTTTGTCCT TTGTTTCCTA CCTTTTGAAT CAGATTCCGT
2401 TTTAGTCAGG AAGACTTCTT GGGACCATTC TTAGTAACCT GAAATTTCTT
2451 TTTTAATTGC ATGAAGTGGA TTGATCATGA GCAAGTGATG GGCTTTATTT
2501 CTCCCTCACT GGTGAATATC CTTTGAACTT GCTGTTTGCA ATATGGGCAG
2551 CCACAAAGGG GGAGAGATGC CTATTAAATC GGCGGGGTGT ATGACTTCTG
2601 AAAACATTGG ATACCCTATT TTGAAAAGGG AAAGGCCCAA TTTGGGGAAA
2651 CATATACCAA TGCATGATTT CTG

FEATURES:

5'UTR: 1-137
Start Codon: 138
Stop Codon: 1569
3'UTR: 1572

FIGURE 1, page 1 of 2

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

	Score	E
CRA|335001098641184 /altid=gi|11360341 /def=pir||T50686 peroxis...	927	0.0
CRA|11000479457833 /altid=gi|6841066 /def=gb|AAF28888.1|AF12330...	834	0.0
CRA|18000005183605 /altid=gi|7504235 /def=pir||T22688 hypotheti...	432	e-120
CRA|1000682325160 /altid=gi|7499323 /def=pir||T21074 hypothetic...	377	e-103
CRA|89000000196990 /altid=gi|7294582 /def=gb|AAF49922.1| (AE003...	348	9e-95
CRA|150000075553401 /altid=gi|9758252 /def=dbj|BAB08751.1| (AB0...	339	5e-92
CRA|335001098657884 /altid=gi|11358611 /def=pir||T49871 peroxis...	330	2e-89
CRA|163000046661776 /altid=gi|10176874 /def=dbj|BAB10081.1| (AB...	326	4e-88
CRA|105000014652720 /altid=gi|10798831 /def=dbj|BAB16462.1| (AP...	200	3e-50
CRA|335001098655048 /altid=gi|11277065 /def=pir||T47703 Ca-depe...	199	6e-50

BLAST dbEST hits:

gi|10145202 /dataset=dbest /taxon=96...	1108	0.0
gi|1437155 /dataset=dbest /taxon=9606 ...	801	0.0
gi|10333851 /dataset=dbest /taxon=96...	745	0.0
gi|8469752 /dataset=dbest /taxon=960...	363	8e-98
gi|11684041 /dataset=dbest /taxon=96...	307	4e-81

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10145202 Placenta Choriocarcinoma
gi|1437155 Retina
gi|10333851 Uterus leiomyosarcoma
gi|8469752 Breast
gi|11684041 Ovary fibrotheoma

Expression information from PCR-based tissue screening panels:

Leukocyte

FIGURE 1, page 2 of 2

```
  1 MLRWLRDFAL PTAACQDAEQ PTRYETLFQA LDRNGDGVVD IGELQEGLRN
 51 LGIPLGQDAE EKIFTTGDVN KDGKLDFEEF MKYLKDHEKK MKLAFKSLDK
101 NNDGKIEASE IVQSLQTLGL TISEQQAELI LQSIDVDGTM TVDWNEWRDY
151 FLFNPVTDIE EIIRFWKHST GIDIGDSLTI PDEFTEDEKK SGQWWRQLLA
201 GGIAGAVSRT STAPLDRLKI MMQVHGSKSD KMNIFGGFRQ MVKEGGIRSL
251 WRGNGTNVIK IAPETAVKFW AYEQYKKLLT EEGQKIGTFE RFISGSMAGA
301 TAQTFIYPME VMKTRLAVGK TGQYSGIYDC AKKILKHEGL GAFYKGYVPN
351 LLGIIPYAGI DLAVYELLKS YWLDNFAKDS VNPGVMVLLG CGALSSTCGQ
401 LASYPLALVR TRMQAQAMLE GSPQLNMVGL FRRIISKEGI PGLYRGITPN
451 FMKVLPAVGI SYVVYENMKQ TLGVTQK
```

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

254-257 NGTN

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 2

1	229-231	SDK
2	475-477	TQK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 8

1	22-25	TRYE
2	65-68	TTGD
3	121-124	TISE
4	157-160	TDIE
5	170-173	TGID
6	179-182	TIPD
7	185-188	TEDE
8	227-230	SKSD

FIGURE 2, page 1 of 4

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 16

1	52-57	GIPLGQ
2	119-124	GLTISE
3	171-176	GIDIGD
4	201-206	GGIAGA
5	202-207	GIAGAV
6	245-250	GGIRSL
7	253-258	GNGTNV
8	283-288	GQKIGT
9	295-300	GSMAGA
10	322-327	GQYSGI
11	326-331	GIYDCA
12	359-364	GIDLAV
13	392-397	GALSST
14	399-404	GQLASY
15	442-447	GLYRGI
16	446-451	GITPNF

[5] PDOC00018 PS00018 EF_HAND
EF-hand calcium-binding domain

Number of matches: 3

1	32-44	DRNGDGVVDIGEL
2	68-80	DVNKDGKLDFEEF
3	99-111	DKNNDGKIEASEI

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	292	312	1.053	Certain
2	345	365	0.613	Putative
3	381	401	1.544	Certain
4	446	466	0.733	Putative

FIGURE 2, page 2 of 4

BLAST Alignment to Top Hit:

```
>CRA|335001098641184 /altid=gi|11360341 /def=pir||T50686 peroxisomal
          Ca-dependent solute carrier [imported] - rabbit
          /org=rabbit /taxon=9986 /dataset=nraa /length=475
         Length = 475

 Score =  927 bits (2371), Expect = 0.0
 Identities = 454/477 (95%), Positives = 466/477 (97%), Gaps = 2/477 (0%)

Query: 1   MLRWLRDFALPTAACQDAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAE 60
            MLRWLR F LPTAACQ AE PTRYETLFQALDRNGDGVVDI ELQEGL++LGIPLGQDAE
Sbjct: 1   MLRWLRGFVLPTAACQGAEPPTRYETLFQALDRNGDGVVDIRELQEGLKSLGIPLGQDAE 60

Query: 61  EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
            EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL
Sbjct: 61  EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120

Query: 121 TISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTI 180
            TISEQQAELILQSID DGTMTVDWNEWRDYFLFNPV DIEEIIRFWKHSTGIDIGDSLTI
Sbjct: 121 TISEQQAELILQSIDADGTMTVDWNEWRDYFLFNPVADIEEIIRFWKHSTGIDIGDSLTI 180

Query: 181 PDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQ 240
            PDEFTE+E+KSGQWWRQLLAGGIAGAVSRTSTAPLDRLK+MMQVHGSKS  MNIFGGFRQ
Sbjct: 181 PDEFTEEERKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKVMMQVHGSKS--MNIFGGFRQ 238

Query: 241 MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGA 300
            M+KEGG+RSLWRGNGTNVIKIAPETAVKFW YEQYKKLLTEEGQKIGTFERFISGSMAGA
Sbjct: 239 MIKEGGVRSLWRGNGTNVIKIAPETAVKFWVYEQYKKLLTEEGQKIGTFERFISGSMAGA 298

Query: 301 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI 360
            TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILK+EG GAFYKGYVPNLLGIIPYAGI
Sbjct: 299 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKYEGFGAFYKGYVPNLLGIIPYAGI 358

Query: 361 DLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 420
            DLAVYELLKS+WLDNFAKDSVNPGV+VLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
Sbjct: 359 DLAVYELLKSHWLDNFAKDSVNPGVLVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 418

Query: 421 GSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK 477
            G+PQLNMVGLFRRIISKEG+PGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK
Sbjct: 419 GAPQLNMVGLFRRIISKEGLPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK 475


>CRA|11000479457833 /altid=gi|6841066 /def=gb|AAF28888.1|AF123303_1
          (AF123303) calcium-binding transporter [Homo sapiens]
          /org=Homo sapiens /taxon=9606 /dataset=nraa /length=411
         Length = 411

 Score =  834 bits (2132), Expect = 0.0
 Identities = 409/410 (99%), Positives = 409/410 (99%)

Query: 8   FALPTAACQDAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG 67
            F LPTAACQDAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG
Sbjct: 1   FVLPTAACQDAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG 60

Query: 68  DVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA 127
            DVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA
Sbjct: 61  DVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA 120

Query: 128 ELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTED 187
            ELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTED
Sbjct: 121 ELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTED 180

Query: 188 EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI 247
```

```
            EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI
Sbjct: 181 EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI 240

Query: 248 RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY 307
            RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY
Sbjct: 241 RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY 300

Query: 308 PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL 367
            PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL
Sbjct: 301 PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL 360

Query: 368 LKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 417
            LKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA
Sbjct: 361 LKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 410
```

```
 Score = 80.0 bits (194), Expect = 6e-14
 Identities = 80/388 (20%), Positives = 156/388 (39%), Gaps = 59/388 (15%)

Query: 95  FKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV--DGTMTVDWNEWRDYFL 152
           F++LD+N DG ++  E+ + L+ LG+ + +   E I  + DV  DG +
Sbjct: 21  FQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKL------------ 68

Query: 153 FNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTST 212
                D EE +++ K                    + EKK     ++ L          +
Sbjct: 69  -----DFEEFMKYLK------------------DHEKKMKLAFKSLDKNNDGKIEASEIV 105

Query: 213 APLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAY 272
              L  L + +    ++    +I       V     R  +  N    I    E  ++FW +
Sbjct: 106 QSLQTLGLTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDI----EEIIRFWKH 161

Query: 273 EQYKKL---------LTEEGQKIGTFER-FISGSMAGATAQTFIYPMEVMKTRLAV-GKT 321
                +          TE+ +K G + R  ++G +AGA ++T    P++ +K  + V G
Sbjct: 162 STGIDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSK 221

Query: 322 GQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSV 381
              I+   ++++K  G+ + ++G   N++ I P   +    YE  K          ++
Sbjct: 222 SDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKL----LTEEGQ 277

Query: 382 NPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLFRRIISKEGIP 441
             G       G+++     Q   YP+ +++TR+   A+ +       +    ++I+  EG+
Sbjct: 278 KIGTFERFISGSMAGATAQTFIYPMEVMKTRL---AVGKTGQYSGIYDCAKKILKHEGLG 334

Query: 442 GLYRGITPNFMKVLPAVGISYVVYENMK 469
             Y+G  PN + ++P  GI   VYE +K
Sbjct: 335 AFYKGYVPNLLGIIPYAGIDLAVYELLK 362
```

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00153	Mitochondrial carrier proteins	305.4	3e-88	1
PF00036	EF hand	50.7	1.7e-12	3
PF00404	Dockerin domain type I	9.7	0.26	1
PF01978	Protein of unknown function	2.7	9.5	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF00036	1/3	27	51	..	5	29	.]	18.7	0.002
PF00404	1/1	67	85	..	1	22	[]	9.7	0.26
PF00036	2/3	61	87	..	3	29	.]	19.7	0.001
PF00036	3/3	90	118	..	1	29	[]	17.2	0.0051
PF01978	1/1	110	121	..	1	13	[.	2.7	9.5
PF00153	1/1	193	472	..	1	313	[]	305.4	3e-88

FIGURE 2, page 4 of 4

```
   1 AACCCATGTT AGTGTGCAGT TCTGCTGGCA CACACATGCA GTTGTGTAAC
  51 CACTACCACC AAAAGCAAGA TGTAAAATAG CTCCATCACC CCCACAAGCC
 101 TTCTGATGCT CTTTTGTCAT CAATTCCCTT CCCGCTAGTC ACAACTGGTA
 151 ACTACTGATT TGTTTTCTGT CCCTATAGTT TTGCCTTTTC CAGAATGTCA
 201 TTGTTGACAG GTATCAGTAA TTCATTCCTT TTTATTGCTA ATTACTATCT
 251 CACTGTATGA ATGCAACACA GGTTGTTTAC CAGTTCACCC GTTAAAGAAC
 301 ATTTTGTTTC TGCGCTTGAC AGTTATGAAT AGAACTGCTA TAAACCCTCA
 351 AGTAAAAGTT TTGGTGTGAA GATAATTTTC TCAGCAAAAA CGCTGACAGG
 401 TAATTTTTCT AAGTATTACT TTTTTAAAAA AGTAAAATAG CCTGTAGCCC
 451 CAGCTACTCA GGAGGCTGAG GCAGGAGAAT AGCTTGAACC CAGGAGGCGG
 501 AGGTTGCAGT GAGTTGAGAT TGTGCCACTG CATTCCAGCC TGGGCGACAG
 551 AGCTAGACTG TCTCAAAGAA AAAAAAAAAA AATAACAAAT AAATAAAAAG
 601 TAAAATGAAA GCATGTAAGT GTAAGATGAC TAGTTCAAGC AACCTCTCTT
 651 CAAGTACAGA GTATTCAGAG TAGAGATTAA AAGAGGTTTT CAAGGACAGA
 701 GAAAATTTGA AGTTTGAAGG CAGTTCCAAA GGAAGGCAAT GATTCTTAAT
 751 AAGACTGGAA GTTGGAAGTA ATATAAAAAG ATAAATCAGT TTCAAGATGA
 801 TTTTACTAAG CAGGCAGCCC TTAATTTACA AATTCTAGAT TCATACATAT
 851 CTTAAACATA CAAAATGATA TGAGGAGAGG TAAGTTCAGG GTCTGAGTTC
 901 CTGGCTGTTG TTGGAACTGA TTTCTGTGTA GTGATTCAGA AGATGTGAGA
 951 CACCCTAATT TACAAGTACA GAGGTATCTT CTTTTCTGCA AACAGCAGTA
1001 CAACAATAGT TCCTCTTACG CAGCTGTGAA TGAACAGGAT TATTACAATT
1051 AATGATATCT CATTTGATTG GCGCCTTAGA GAATTAAGAC CTTTCACACC
1101 TAATATACAA CTTTGTTGTG AAGGCAGATA TTTATATTCT CATTTTACTG
1151 ATGAGAGACT ACCCGGAGAC GCTATGTCAC ACCTGAAGGA TTAGGTACTT
1201 TCTCTGTTAA GTCCAATGTT CCTTCCGTTA TTCCATGCTA GGCAGTAATA
1251 AGTTCTGTCT TGCCTGAGTA ATAAGCTCCA AACCTCGGAA CTGCACCCAT
1301 CTTGAGAAGG AGGAGGGCGC TGTGGTTTTT TCTGATAAGT GCAGCTGGCA
1351 GACACTCTAT ACGCTTAATC ACGGGCAAAT CCTACCTAAG CTGCCTACCA
1401 AACTAGTCCT TCTTTTCCCC GTTGCCCACG CAGATGGCTG TTGATCTTTT
1451 CTGCAACAAA TCCAGGAGTT TCTCCTTTTT GTTTTATAAT TGCTCCAATA
1501 GATGCTTTAG GATTTAACTC TCTGCTTTTT AAAGCAGAAT CGCCATCCCA
1551 GGTGTGCAAC CACGAAAAAA TTAGACATCC GTGAGAGACA ATGCCCTCCA
1601 TGGCCCAGTT TCCAGGCAGA GAGAAGCAGC TCTGGGCTGA CCGCCAAGGC
1651 TCCGGCCCGA GAGGGTCTTT AAGTGGAGTA ACCAGTCTTC AAGACCCCGC
1701 TCCCAAGCCA CCGACGCGCT GACGCTGCAG CCCTGGACCT GCTGGGGGCC
1751 TCTTCCTCGG ACCCGCATGC TGACAGCGGG ACTGGCAACT GGGCAGAGGT
1801 CGACCCCGGG TCCGCACAGC ACCTCCCGAG ACCCAGCTCC CAGCTCCCTC
1851 ACTTCCGGCT CTCTGGAGGC GGGCCCGGCC AGTGCCGCCG AGGCCAGCGC
1901 GGCGAGCTCC TCCCCAGCAG CGGCGGGACG GCCACACCCT GCGCGCCGCG
1951 CGGGCTCGGG TGGGGTCTCC GCTCCTGCGC CCTGCGCGCC GCAGCCGCAC
2001 CCCCGACGGC GCCCCAAACG CTGTTGCGCC GCGCGCCCCG CCCAGCCCGG
2051 CCTCGCGCTG GTCCCGGTCT CGCCCCGCAG CCCTCGATCT CCCGTGACTT
2101 CCTCGGCCAG GCCGCCTGCG CCTCTGGGAC CATGTTGCGC TGGCTGCGGG
2151 ACTTCGTGCT GCCCACCGCG GCCTGCCAGG ACGCGGAGCA GCCGACGCGC
2201 TACGAGACCC TCTTCCAGGC ACTGGACCGC AATGGGGACG GAGTGGTGGA
2251 CATCGGCGAG CTGCAGGAGG GGCTCAGGAA CCTGGGCATC CCTCTGGGCC
2301 AGGACGCCGA GGAGGTGGGT CGCCGCCGGG GCGCCGCCTG AGCGTAGGGA
2351 GGGCTGCGGG CGCTGGGGAC ACTGCGAGGA CCGAGGAGGG CGGCGGCTTG
2401 AGGCGTTGCC AGGAGAGGAA GGAGGAACTG TGGCGCCCAG CGCTCCGGTG
2451 GCTTCAGAAA CTCGGGCGTG GGGCCGCGAC CGGCGACCCC GGTAACAGAA
2501 GTGGGTCATA ATACGAAAGT CTACTGGTAT TTGTCCAGAT AAAATGAGTG
2551 TTGTGGACAC TCTGGCCCAC GGGCACTGTT AAATTTTTAA GACACTTTTG
2601 TCCTGAATCC ATCCCAGGTT CTTTGTTTTC TGTTTTAATA CCTTGCAGAC
2651 ATGTAATCCG TTTTAGCTGT CAGACTTCAG TGGGTCCCAA GTTTTGTATA
2701 AAGGCGCACA CATTCGATCT CTTTCGAAGC TGCTTTGTTA CAGCAGCTAT
2751 GTGTATTGTC TACTGTTTGA AAACTGTTTG AAAACCAATC GCGTGTTTCC
2801 CCCACTTCCT GTTGAGAAGG AATGGCGGCA TTCCATTGTT TAAGACATTC
2851 CTAGGTTAAT GCCCTAGGTA CATAAATTGA TCTGAAGGGT TGACTTGACC
2901 TGCGACTGAG CAATTTCATT TTCTCTGAGT CATCTTAACT GTGCCCCTGA
2951 ACTTCTGCCC CTTTAGTAGG GTGGAGATAT GTGGAACTTC TCCAACCCTG
3001 TTGAAGCGTT CCCTGACACT GGCATTCTCT TATCCAAAGA GGGAAAGTGA
3051 TTAGGTTACT ATGAGGGCCA ACAACTGTTA TATAGTTATA TTTCACTTCT
3101 CTTTTAATGT CTTTGGTAGT TATAGGCCTC TTCAGTTTAC TGTTTCTTCT
```

3151 AGAGTCAGAT TTAGTAAGTT ACAATTTTTT TTGAAACTGC CTGTTCTGTC
3201 CAAGGTTCAT AATACTCACC GATGATTTTA TAACACTTCT GACTGAATCT
3251 GTAGGTAGGT TCTCTATTTC ATTCCTCATA TCTATCCTTT TCTCCCCTTC
3301 AATCTTGCCA AAGTTTTGTG TATTTTATTC ATACTTTGAA GGAACCAACT
3351 TTTGGTACTT TGTGCTGATT GTCCCAGAAA TGGCCCAGTT GGAGTTCCCC
3401 ACCATGTCCA ATCATTGGCT GGAAGCAGCC CAGGAAAGGG ACGACCTTGC
3451 TGCAGTGCAT CAGCAGATGC CAGGGTTAGA GGCTAGAGAG TGGAAGTCAA
3501 CTGTGTTCCT CACAGTAGGT GCCTTTGAAG GGAGATCTCA GTGGTACAAC
3551 TCCATGGTCC CTACAATATA CAAAAGCTCT TTGGAGTGCT CAATGATTTT
3601 TAAGATTGTA AAGGGATCCT GAGATCAAAA AGCTTGAGAA TTGCTGCTGT
3651 ATCACCATTT TTACGTAACT GCATCATATT CTGTTATATG TTTGTGTCAT
3701 AGTATATGTT ACCAATTCTT TTTAAATCAC CTTTTACTTT ATTGATAGTT
3751 TAAAAACGAT TGTAAGTGAA ATTGCAATGG ATGTCCTTTG TATTCATTTT
3801 CTCATTCTGG TCCAGTTACT TTCGTAGGAT AAATTTTGAG GAGTGGACAT
3851 TGCTGAGTCT GAAGGTAACA CACATTTTAA ACTGGGATAC GTATTGCCTT
3901 TCGGAAACCT TAGACCCATT TTCACTCTTT TGACTGACAG TGCTTGCTTC
3951 TCCACATCCT CGCTCATTCA GGGTATCAGT CTTTGTAAAG TCTCCTATTC
4001 TGCAGGTGAA ATTCCTTTTC ATTTCCTGTC TTAGTCCATT TAGTGTTGCT
4051 ATAGTGGAAT ATCTGAGACA GGGTAATTTA TAAAGAAAAG ACATTTATTT
4101 AGCTCACAGT TCCGCAGGCT GGGAAGTTTA AGAAGCGTGG TGCTGGCATC
4151 TGCTGGACTC CTGGGGAGGG CTTTCCTGCT GTGTCACAAC ATGGTGGAAA
4201 GTCAAAGTGG AAGTGGACAT GTGTGAAGAA GCAAAATCCG AGGGGTGTCC
4251 TGGCTTTATA GCAACCCAGC CTCGAGGGAA CTGATCCATT ACTGAGGGAA
4301 CTAATTCAGT CTCATGAGAG AGAGAACTCA CTCACTACTG CAAGAATGAC
4351 ACCAAGCCAT TCATGAGGGA TCTGCCTCCG TAACCCTGAC ACCTCCTGCT
4401 AGGTCCCTCC TCCCAACACG GCCACATCAG GGATCAGACT TCAACATGAG
4451 TTTTTGTGGG GACAAACAAA ACGTAGCACT TGCTTTGCCT TTTGGTTCTA
4501 TTCACATCCT CCACAGGATT GCATTATGCC TACCCATTTG GTGAGGGCAG
4551 TCTTCTTTAA TTGGTTTACT GATTCAAATG CTACCCTCCT CCAGAGACAT
4601 CCTCACAGAC ACACCCAGAA ATCATGTTTT ACCAGTTATC TGGGCATCCC
4651 TTAGTCCAGA CGAGTTGATA CATAAAATTA ACCATCACAC ATGGGATAGA
4701 ATTAGGATTA CACAGTCAAC CTTTATGGGA GAAAATTTCA GAGGCATGTC
4751 AGGGGTTTAT GTAATGTCAA GGAGTGAGGA CATTGGCTAC TTGAGCATAG
4801 AAATGAGAAC TGTGGGGTGA CTCTTCGGTG GAAAGTTTCA AGGTAGTAGT
4851 TTGTATCTAA GCCAAATACT CAGCTTGAAG CAAAATCTCT ATAAATTTTC
4901 ATCTGATTTG ATCTCATCTC CGTGTTTCCA AGCATTTGTA ATGAATTGAG
4951 CATTTAGAAG AGAACAAATT TCTGTTTAAG TTTCTTTAGA TTTTAGATGG
5001 AAAGAATGTA GAAATAAGAG TAGAATGTAG AAATAGGTAT AAAGAATATA
5051 ATAGCTAACC ATTACTAAGT GTTCCAGAAT TATCCAGGGA AGAGAAAAGA
5101 ATTCAAGGCA AGTCCTGAGA CAAAATTAAG AACCAATTGG AAGTGAAAGC
5151 GCTACATTTT TTTTTTCTGG TATGACCTTT CTTTTCTATA TGTTCCAAAT
5201 CTCCTCACTA TGAAATTAGT GAAAAATTAA AGTTAAAAAT TAGAGAAAAT
5251 TCACATTAAG TTCTCCTAGG ACTCAGTAGT ATAAGGGTAT AGACTGAGAG
5301 TAGAATGTAG TGTGAGAACA AGGAGATACA GTATTTAACC ATTACTAATT
5351 CTCTTATACT TGTCTAGTAA TCCTATTTCC TTTTAAAAGT CTTCAGTTAT
5401 TTTCTCTTTA CGCACCTCCT TCTCCCTCTT GTCTTCCTCC TTCTACCCCC
5451 ATCTTTCTTC CTGTGGAGCC TTCATGAATG GGATTAGTGC TTGTATAAAA
5501 GTGACCTGGA AGACCTTCCT TGCCCCTTCC ACCATGTGAG GACACAGTGA
5551 GAAAACAGTG GTCCATGGAA CCGGAAAGTG GGTCCTCACT AGACAGTAAA
5601 TCTCCTAGCA CTTCGATCTA GGACTTCCAG TGTCTGGAAC TGCAAGAAAT
5651 CAATGCTTAT TGTTTAAGTA AGCCAGTAGT ATTTTTGTCA TAGCAGCCCA
5701 GTTGGACTAG GACAATTACC AAGAGCAAGA AGGGAAGCAG CAAGCTACAA
5751 GAGAGTTCCG TCCTTGGTGT AAATTGACCG TGTAATCCTT GTCAAGTTTG
5801 AGCCTTACTG GAGCTTTACT TTCTTATTCT TAAAATGCAG ATATCTTGCC
5851 TGCATCCTGG ACAGAGCTTT TAACAAGGTC ATATGTTGCA GAATATGAAA
5901 GTTCATGTTA AAAAACCCTT TAAAATGTGG TATCCCATTT ACTAGCTGGT
5951 GAACTTCTTG AGGAACCTCT GTGCCCATGG GTATGAAGTG TATGCTGAAT
6001 GATCACCCAA TGTTAGAGGA GTGGGTGGAC TGGTAACCTG ATTTAAGGGC
6051 CATTCTAACT CTTACATTCT ATGATTTTTT TAATTCTGTC TTTAAGTTTT
6101 TACATTTACA ATCACAGAAA AAATAGTCAC ATAGAAGAAT AGTAGCTTAG
6151 CAAATGTTTA TTGCATTGAG TGGAATCAGG ATTTCACTCC ATTAAGTAAT
6201 TCCTCTGTTA ACAAAGAGGG TTCATTTCAT TTTTATTTCA TTAATATTGC
6251 TTTTTTTTTT TTTTTTCTGG AGACAGAATC TTGCTCTATC ACCAAGGCTG

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6301 GAGTGCAGTG GTGCGATCTC GGCTCACTGC AGCCTCTGCT TCCTGGATTC
6351 AAGCGATTCT TGTGCCTCAG CCTCCCAAGC AGCTGAGATT ACAGGCACAT
6401 GCCACCACAC CTGGTTAACT TTTGTATTTT CTAGTAGAGA TGGGATTTTG
6451 CCATGTTGGT CAGGCTGGTC TTGAATTCCT GGCCTCTAGT GATCTGCCTG
6501 CCTCTGCCTC TGAAAGTGCT AAGATTACAG GCATGAGCTA CCATGGCCAG
6551 CCCATTTCCT TAATATTTTA ATTGTCAGAC ATGTTATGGT TTCTGGCACA
6601 ATATTAAGAA GACATGATAT GAAATCACAG GGTGAATTTT AGGGCATCAC
6651 AACAGAAAGA TTATGGTATA AGAAAAACAA TGGAATTCCA ACTACATTTC
6701 TGTCAAATGT TCTAAAATAT ATAAAATCTG TATCTTTTGT GTTCTCTCCT
6751 GATTTATATT CTAAATTTGA TGTTATCCTT CTCTGCAGAA ATAAAGTGTC
6801 TGAAAGAATG AAAAAAATGG AAGAATTCTT TAGTAAGGTA TAAAATACCC
6851 TTTCTATCTT TGTAGCATTC TAAGCCTTTT GTCACCTTTC CAAACTCCCA
6901 ACATGCCATA TTCCCTGACT AGGCCACAGC CATGTACATT GATCCCTTTA
6951 TTTTCTTCTC TCTGCCTGAG ATTTCTCTCA TTCCCCCTTC TCTGCCTGGT
7001 ATATGATTGC CCATTGTTTA AGGCCCCAAC TCACCTTTAT AATCTTCCTA
7051 GCCCACTTTC TTTATCGGTA TTCCAGAAAA AACAAAAGAA GCTTCCACAA
7101 GACAACATTC TGTAATACAC TGCTTAACTT CTTTTGACCC TGCTGAGTTC
7151 AAAAATCTTA TCTTTTTAAG GATTGAATGG AGTCCACCAA GGTATCTATA
7201 TTTGACAGGA TTTATGAAAA CAAAAGGATT TGTTGAGAAA GTTTGAAGCC
7251 TAACTCTGAA ACGTGGATCA TAGTGTTTAC TACACATTAA CTGTTTTAGT
7301 GGATGTAATA GTTATTATTA TAGGCTGTGG AATCAGAACA GGGTTCAAAT
7351 GTTTTCACCG CTTGCTAGAC TGTGGCCTTG GGCATGTTAT TTAATGCCTG
7401 GAGGCCTCAA ATGTTAACTA GGAATGGTAA GACCTACCCA GTAACTTAGC
7451 ATAAATAGTA AATTCATTCA TTTAATGTTT TCAAACAGTG CCAGACATTG
7501 TTTAATGAAC TGGGGATATA GTGGTGAACA ACACTGACAG CGTTCTTCAT
7551 TGTATTCTCA AAACCCTCCC TATAGTAAGT AGGTCTGTGT GTGTGTGTAG
7601 GTGCATGGGG AATAAAAAAT AATAAGCAAA TAATGAACAG GGTAATTTCA
7651 AAAAGCAGAA AGAGCTATTC AACAAAACTA CCTGCCTTTT ATTAGATGAA
7701 ACTCTCAACT CTATGGTTTG TTCTCTCCTG TCAATTCTGT TAAATGCTGT
7751 CAGCCTGTTT TCCTTATCAC CCTGGCCACG ACTTCTGTCT TTTCTGCTTG
7801 GTCCTGTAGA CTCTAACCCA AGGCTCATTC TCTGCCTGGC TATCTGCCTT
7851 CTGTGGCTCT TTGCCACTAC CTACATTTTC TGTGTTGCAC AGGGAAGGAC
7901 CATTCCCTGT GGACCATAAA ATTCTCTTTT TGAAAGAATT CATTCTTGAT
7951 TGGGCCACAG CACATCTTGT GAAACAGCAT TAGACATTTG CCACTGCTCA
8001 GCAGCTCTGG GGGAAAATGT TTACTGAGAA GCGTACAGTA GTTTTTTTGA
8051 CTAACCATGG TGCAACCTCC TCCCAGAGGG AAACCTATGA GTATTTCAAG
8101 GACATGTGAT GGTCTGTTTT TGTCCCCAGT ATCTGACATG ATGGGTAGTG
8151 TAGAGCAAGA GCTTACAGAT AATGGCTAAA TTAAATTTTC TTTTTGAATT
8201 TTAATATTCA ACTTTTTAGG GTACCCAATC TCCATATTTA GGAAAATAAA
8251 TTACATAAAA AGTGGAGAGT TTTTATTGTG AAACTGCACC TCCATATTCC
8301 CAGTGGTGCA GGATGAGGGA GCACAGGTGT TGGTCTGGGG AAGCCAGGGC
8351 CCTCTGTGGT TCTGGAGGGT GAGGATTAAG AGGAAGCCTT AGATAGTATT
8401 TATGAGTATC TGCTGACTTC TCTCTGGGAC CCAAGATCAC TGAACTTTTG
8451 CCTATTTTGA GATCATCTTT CCAATCCAGC CACTAACAGC TGAAGGATAG
8501 GCTTGCCCTG GAGCCATTGT AGTGGTTGGA TGAAGATAAA AGATAAAAAA
8551 CTGTGAGGGG AGGTGTCACA GAAGAAAGGG CCCATGTGGG CAGATTTTCA
8601 TTCAATTCCT AGTCTTTATT ACAGCAATTC TCCAGTGCTG CAACCTTAGA
8651 AAAGGATTCC TACAACACAA TGTAGGTACC CATCAGCAGC AGATTGGATA
8701 AAGAAAATGT GGTACATACA CACCATGGAA TACTATGCAG CCATAAAAAA
8751 GGAGCAAAAT CATGTCCTTT GCAGCAATAT GAATGCAGCT GGAAGCCAAT
8801 AACTTAAACG AATTATTGTA GAAACAGAAA AACAAATACT GTGTTCTCAT
8851 TTACAGGGGG AGCTAAACCT TGGGTAAATG GGGCATAAAG ATGGGAACAA
8901 TAGACACTAG GGACTCCAAA AGGGGGGAGG GAGGGAGGAG GGCAAGGGCT
8951 GGAAAGCTTC CTACTGGGTA CTTTGTTCAC AACCTGGGTG ATGGCACGAT
9001 TAGGAGCTCA AACCCCAGTA TCACACAGTA TACCCTTGTA ACAAGCTGAT
9051 GGTGTAACCC CTGAATCTAC AATAAAATTA TTTTATTTTA AAAAATCATT
9101 ATAAGGATTT TTAAAAAGAA GGATTCCTAG ACAGGTGCAG CCAAACAATT
9151 TTTTTTAAAT GTTGGCAGGC CGCCACCGCC AGTCACTTAT GCTGCAATAG
9201 CCCATGTCCC AACATTCCCA ACCTACTTCT CTCCAAAAGA GAAGCTATAC
9251 TTTCAGATGG CCCTGTGCTG GGTTCTCCCT GGAAGTTTCT GGGGAAAGGG
9301 GCTTGAGTTG CCCCGACTGG ACTCTTCCTG GAGTGGGAGC CGGGGCTTCT
9351 GATCAGACGT GAGTGAGGCA GGAACTCCGC GGTCTCCCAG CGCAGCCCAG
9401 AGTGCGGTCC CACGCAGGTC CCGGGTCCTG CGCGCTCGCG CCTTTGCGCT
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9451 GAAGCCGTTA GGATGAGCCC TCTCCTTCCA GAGCTTTAAC CGATGAAGGT
9501 GCATTGTGTT TGGCGCCCCT GAGGAGGATG CTGTCTTAGG CCTCTTCCCA
9551 CTGGACGTGT GTGGTGGGCA GAGATCCCGT TCGTCGGTCG CACTTCCACC
9601 CCGCTGGGGC TCACTCAGGC CGCGGAGCTG CGAGGGAGAC ATCCTCGATG
9651 GACTCCCTCT ACGGAGATCT CTTTTGGTAC CTGGACTATA ACAAGGATGG
9701 GACCTTGGAC ATTTTTGAGC TTCAGGAAGG CCTGGAGGAT GTAGGGGCCA
9751 TTCAATCTCT AGAGGAAGCG AAGGTGGGTC TCACTGGGGC TGTAATCAGA
9801 GAGACGTTGG GGCTGGGAGC CCTGGAGAGG CATTGGGCAG AGAGGGCAAA
9851 ATTTACATGT TGTCAAGCTT GACCTGGGCC CACTGCAGTG TTCAGGTGGT
9901 TGACCAGCGT TACCGTTTAT TAAGAATAAC AACACAGCTA ACACATTTCT
9951 CAAGTATTTT TCTCCGTTTT CTCCTTGGCT GTAGTAAAAT CTCCAACTTC
10001 AGATTGCTCT CAAGATGTTG GCTACATACA GCCTTGTCTT AGGAGTCACC
10051 TTGTTCAATG TGCTCACCTG TCATTAGTCA CCCAGAGGGG CGTCTAGGCT
10101 AAAGATGCGC CCTCCCCAGT TCAGAGAACT GGAATAATCA CTCTACGTGT
10151 ATTTGGGAGT GGGGTGGTGA TTGGAAATTT TCTGATGTTA TGTTTTGGTT
10201 TCTGTTCCTG GAAGGGGGCA GTGGAAGTGG CTTTTACTCT CGGGTTTCAC
10251 TAGTGCTGAG GTTTCCTCAT AATATGCCTT AATTGATAGA CCCTAGTTAT
10301 CAGTACCGAG CTTAGGCTAA CCCTTCTCTT CCCCAGAAGG CTAACCTACA
10351 GGCTCCTTCT CAGCATGTTG TGCTTCGTAC ATACTCCTAT TGCAGTATTT
10401 CCAAGTCATT TTTCATTTGG AATTTATTAT TGTATATAAT AATTACTTTA
10451 TAAGTATATT TGCTCTTTGG ATGTTTGACC CGGTAGACTG GGAGATCATG
10501 AGCATGTGGA CTATTGAGTT TATTTTGGAT AATTGGTACT TCGTGCCCAA
10551 AAAACTGTCA GTTGAGTTCT GTCATGTTGA AATTTAGTAA AACTCTTTCT
10601 ATTAGCCATG TGAACTTTGG GAATATTGAA GCATCCATTC AGTCATGGGT
10651 CAGTTCTAGT TTGAGCACAT TCTATATTCC AAGCCCCATA CCCTGGTATC
10701 CTCATCTGTT ATATCAGAGG CCTGGACTGT GTACTTTCTG TGGACCAATT
10751 CAGTCCAAAA TGTTATTTCT GCAAAGCTTA TCTGGATTTT TAATTCCTAG
10801 AAAAAAGCAG TGTTTCTCCT TTTAAAGTTA AGTGTTCTTG TTCAGGTGCA
10851 GTGGCTCATG CCTGTAATTC CAGCACTTTG GGAGGCCAAG GCAGGTGGAT
10901 CACTTGGGGT CAGGAGTTCA AGACCAGCCT GGCCAATATG GTAAAACCCC
10951 ATCTCTACTA AAAATGCAAA AATTAACCGG GTGTGGTGGT GGGTGTGTGT
11001 AGTCCCAGGA GGCTGAGGCA GGAGAATCAC TTGAGCCTGG GAGGCAGAGG
11051 TTGCAGCAAG CTGAGATTGC ATCACTGCAC TCCAACCTGG GTGACAGAGT
11101 GAGACTCCAT CTCAAAAAGA AAAAAAAAAA GTTAAGTGTT CTTCATATTT
11151 GTTTAAAGAC ACTCTTATAT TTAGATTTGC AAGTGTAAGT TGTATTTGTT
11201 TATTTGATAC AAACTAGCCT TTCATAAGAA ATTCTGGGTT AGCTATCAAG
11251 TCGAATCTTT TGAAACACAT TTCTTCCTTA TTGAAACAAA AGGTTTGTAG
11301 AGCTGTCTTG CATTTTTGGC AAGGACGCTT TGTGTACCTA GTGGTGACTG
11351 AGGAGGGTTC ACATGTCAAA ACCCAAGGGA GGGGTGTCCC CAGAGAATTC
11401 TGCACCAACC ACACAGAACA TTCTGTTTCA GAGGAGCACC ATTGTGACTT
11451 TTCCTCAAGT GGCAGTCACA TCGTTAGGAG GTTTTGATGT GAGGTCTCTT
11501 CCCACACGTC TCCACCTCCC CAGTAGGAAA ATTTGTTTAT ATAGACAAAA
11551 CTCAACTGAT TAAAAAAAAA AAAAAGAAAT GATACTTACA TTGTCGTGTT
11601 AAGATACAAA AGCAATAACT TTTTATTGTG AAAATAGTCT GTTTTTGAAC
11651 AATATATTGT TTTGTTTTTT CCTGTGAAAG TTGAGAAACT AAATATACGA
11701 AGAGATAATG GTCAGACCAT AAATAAAAAT AGAACTTTGA CTCAAAATTT
11751 ACAGCAGTCT GCCCAGAAAA CCAGCCCTTT ATCTAAAATA AACAGACCAG
11801 GAAACCAGCC TGTTATGTCA GACTTATAGG AAGTCAGGTT GCTATCTCTA
11851 GAGACAATAC ACAAAGCTAT GCAATAACTG CTGTAACAGC CCCAAATGGT
11901 CAGAATTTGA TTAATAACCG ACAGCCCCCC TAATTTTTTT CTTCACTNNN
11951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNTTC
12001 ACCGCTTGCT AGAACTGTGG CCTTGGGTCA TGTTATTTAA TGCCTGGAGG
12051 CCTCAAATGT TAACTAGGTA ATGGTAAGAC CTACCCAGTA ACTTAGCATA
12101 AATAGTAAAT TCATTCATTT AATGTTTTCA AACAGTGCCA GACATTGTTT
12151 AATGAACTGG GGATATAGTG GTGAACAACA CTGACAGCGT TCTTCATTGT
12201 ATTCTCAAAA CCCTCCCTAT AGTAAGTAGG TCTGTGTGTG TGTGTAGGTG
12251 CATGGGGAAT AAAAAATAAT AAGCAAATAA TGAACAATAA AATTATTTTA
12301 TTTAAAAAAA AAGAAATGAT ACTTACATTG TCGTGTTAAG ATACAAAAGC
12351 AATAACTTTT TATTGTGAAA ATAGTCTGTT TTTGAACAAT ATATTGTTTT
12401 GTTTTTTCCT GTGAAAGTTG AGAAACTAAA TATACGAAGA GATAATGGTC
12451 AGACCATAAA TAAAAATAGA ACTTTGACTC AAAATTTACA GCAGTCTGCC
12501 CAGAAAACCA GCCCTTTATC TAAAATAAAC AGACCAGGAA ACCAGCCTGT
12551 TATGTCAGAC TTATAGGAAG TCAGGTTGCT ATCTCTAGAG ACAATACACA

12601 AAGCTATGCA ATAACTGCTG TAACAGCCCC AAATGGTCAG AATTTGATTA
12651 ATAACCGACA GCCCCCCTAA TTTTTTTCTT CACTTCCAAC TTAGGACGAA
12701 CCAGAGAAAG CTAAATATGC ACCACCTACT AATCAAATAG GGTGCCGCGT
12751 TTCTAATGAA CCCTCCTACA GCTTCCCCAG GCCAGCAGCC CCCAATCAGG
12801 AAACGCCTGA AGCCTTCCCT TTTTCTCACT GTAAAGCTTT CCCACTCCTC
12851 TGCCTGGCTT TGAGTCTCTG TCAATACACA AGTGAGGGTG TCTGACTCCC
12901 TTGCTATAGC AAACTCGGGC CAAGTAGATT TTACTTTTCT CATTTGATTG
12951 GTCTTTTATT TCTAGAAGGA ACATACAAGA AAATTTAAAG GGGAATCCAT
13001 TCCTAATCTT TCATATTATA GTAGTCCCCT TTTATCTGCA GGGCATATTT
13051 TCCAAGACCC CCACTGAATA CCTGAAACTG TGGGTAATAT TGAACCCTAT
13101 ATATACTCTC TCTATATATA CATATATATA TATATTTTTT AATTTTTTTT
13151 TACTTTATCT TTAATTAGCT TTAGCTCTTT TTTTTTTTTT TGAGATGGAG
13201 TCTCACTCTG TCACCCAGGC TGAGTGCAGG GGTGCAGTCT TGGTTCACTG
13251 CAACCTCTGT CTACCGGGTT CAAGCAATTT CTTGTGCCTC AACCTCCGGA
13301 GTAGCTGGGA CTACAGGCGT GTGCCACCAC TTCCTGGCTA ATTGTTTTAA
13351 ATTTTAGTAG AAACGGGATT TCACCAAGTT GGCCAGACTG GTCTCGTACT
13401 TCTGACCTCA AGTGATCCGC CCACCTTGGC CTCCCAAACT GCTGGGATTA
13451 CAGGCGTGAG CCACCATGCG CCCAGCCATA GACTATATAT TTTTGATCTG
13501 ATAACTGGTT CAGCTACTAA GTGACTAACA GGCAAGTAGC ATCTATAGTG
13551 TGGATATGCT GGACAAAAGG ACATTCACCT CCTGGGCAGG ATGGCACAGA
13601 ATGTTGAGAG ATTTTATCAT GCTACTCAGA ATGGTGTGCA ATTTAAAACT
13651 TATGAGTTGT TTGTTTCTGG AGTTTTCCAT TTAATAGTTC AGACCATGGA
13701 TTGACCGCAG GTAACTGAAA CTGTGGAGAG TGAAACTGTG GATAAGGGAG
13751 GACTATTGTA TTGTTAAGTC AGACTCATTA GGCAATCATA ACTCTTGATT
13801 TGCCATCAGA AATGCTGCAG AAATATGGGT TAAAAAAAAC TGTTCAAAAA
13851 TAGGGTCAGG GATGTCCTTT AACTTGTTAC TTCCAAAATG TTAGTGAAAA
13901 CTGTGGCCCC AAAGAGTGAA AGGAACAAAT GACTAAGAGA AAATCTTGTT
13951 TTCAGGATGA CAGATTAAAA AAGAAGCAAC TTGCTGAAAC ACTGAAAATC
14001 TCTCCACTTG TAAGATAACA CAAAACTGGC TAAAACTGGT TGGAATGAAT
14051 ATGGCCAACT CAAGTCTGCA CAGAACTAAC TTGGTGATGT TACAGCCCAA
14101 ATTTCCACCA CATATTTTAT ACTAACTCCC CCCGGATTTT CACACATGAT
14151 CTGTGAGGTA GCATGAAGAG GTAACTATGC ATGCCTAAGG ACTTGGGAGA
14201 CCTCCCCATT TCCTTCCACC AATCACCCAC TAATCCCAGA ATCCGCCCCC
14251 AAACCTTTTC TAATAACTAC CTTAAAGCCA GCATAGGGAG ACAGATTTGA
14301 GCTGGACTCC TGTCTTCTTG TGGGTCACCT TGCAATAAAA AGCTTTTCTT
14351 TTCTCAACAC CTGGTATTAT AGTATTGACT TCTAGTTCAT CGGGCAGCAA
14401 GCCCCTTTTG GTCGGTGACT ATTCTTGTTC GCTGATATTT CCATTGGCCA
14451 AAATATAAAC CTCTTAGATG AAACTTCAGT ACGTAAATGG CGCCACAGAA
14501 TGCTGTGACA TTTTTCTCTT GGATTATAGC AGGTTACTTT ACTGAATACC
14551 GTAGGCAGTT ATAACACACT AAGTATTTGT GTATCTAAAC ATAGAAAAGA
14601 TACAGTAAAA ATATGGTAAT TTTTTTCAAC TTTTAGTTGA GATTTGGAGG
14651 GTATGTGCAC ATTTGTTACA AGGGTATATT GCATGATGCT GAGGTTTGGG
14701 GTACAATTGA ACCCTGTCAC CCAGGTAGTG AGCATAGTAC CCAATCGATA
14751 ATTTTTCAAC CCTTGTCCAT TCCCTCCCCG TTCTTGTAGT CCCCAGTTTC
14801 TGCTTTTCCC ATCTTTATAT CCGTGTGCAC CCCATGTTTT GCTCCCATGT
14851 GTATGTGAGA ACTTGTGGTG TTTGGTTTTC TATTTCTGCG TTGATTCGCT
14901 TAGGATAATG GCCTTCAGCT GCATCCATGT TGCTGCAGAG GACGTGATTT
14951 TATTCTTCTT TATGGCTGTG TAGTATTCCA TGGTGAAAAA TATAGTACTA
15001 TAACCTTACT AAATCACTGT CATATATATG GTCTATCATT GACTGAAATG
15051 TATACAGTGC ATGATATATA TATATATATA TCTATAATGT CTTATCCATT
15101 TCGTGTATTA TGAGATTTGA TTGCTAATAT TTTATACAGG AGTTTTGCAT
15151 CTTTTTCACT AGTTGACATT GCTTGTAATT TTCCTTTTTT TGTGATGTCC
15201 CTGTTAGGTT TTAGAATCAA GTGTATACCC GCCTCATAAA ATGGGTTGGA
15251 AAATGTTCCC ACCCTTTCTG TTCTCTGGAA AATTGGTGTT TTTTTCTTAA
15301 AGTTTGGTAG ACATTATTGT TAAAACCATG GGGTCCTCGA TTTTTCTTCA
15351 TGGAAATGTT TTCAAATTAC ACTTTAAATT TCTTTAAAAT CTGAGTATAG
15401 GGCTATCAGA CTTTCTGCTG TCTTATGTCA GTTTTTAATA AGTTGTTTTT
15451 GTAGGCGTTT GTTATCTCAC TTTCATATTT TTGATATAAA GCTTTTCATA
15501 ATATCATTAA TGTCTATAGT GTCTAGTAGT TTCCATCTTT ACTTTCTGAC
15551 ATTGGTTATT TGCCAGTTTT AGGAGTTTAT CAATTTTATT AGTCTTTTCA
15601 AAGAACCATC TTTTGGCTTT GTTAATCCTC CCAATGGTGT GTTTTCTTTC
15651 TCATTACTTT TTGCTCTTTA TTTCCTTCAA CTTCTTTTTT GCTTAATTTT
15701 AAAATAATTT CTTGAGATTG AGATAAGCCT CAATGATGGG TCACCGATTT

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15751 CCAGTCTTTC TTCTTTTCTA ATTATGCATT TTAAACCAGA AATCTTTCTC
15801 TAAGTGTAGC TTTAGTTGCA GCTCACAAGT TTCAGATCTG TCTCTCAGTC
15851 TGGAGGTTGG AGATCTGACC ATGACCATGA AACCATCCAG TCACAATGTG
15901 GCATTATTTT TTTAATTTTT TTTTTTTTTT TTGAGATAGA GTTTCACTCT
15951 TATTGCCTAG GCTGGTGTGC AATGGTGCGA TCTCGGCTCA CAGCAACCTC
16001 CACCTCCCAG GTTCAAGCGA TTCTTTTGCC TCAGCCTCCC AAGTAGCTGG
16051 GATTACAGGC ATGCGCCACC ATGCCCAACT AATTTTGTAT TTTTAGTAGA
16101 GATGGGGGTT CTCCATGTTG GTCAGGTTGG TCTTGAACTC CCGACCTCAG
16151 GTGATCCGCC CACCTCAGCC TCCCAAAGTG CTGGGATTAT AGGAATGAGC
16201 CACTGTGCCC GGCCCAACTT GGCATTATTT ACCCAGAAGA GCATGACCAT
16251 GAGAACAGTA GAATTTGTAA GCTTTGAGTG GGTGACTATG AGTGTCATAA
16301 TAGGTAGATA GGTTATATTT TGGGTGGTGG TAGGAGAGGG CTTACAGTTT
16351 GCTATGACAG CTTTTTATAT GGATCATCCT TAGTAAAAGA TTATTTAATT
16401 TTTGAAATCA AAGGGGAAAA CACTAGTTTA GGCTTTCTTC TTTCTTTCTT
16451 TTTTAGAGAC AGGGTCTTGC TCTGTCACCA GGTTAGAATG CAGTGGTGCA
16501 ATATTGCTCA CTGTAACCTC AAATTCCTGG GCTCAAGTGA TCCTCCTACC
16551 TCAGCCTCCA AGTAGCTAGT ATTTACAGGC ATGCACCAAC ACATCTGGCT
16601 AATTTTAAAA ATTTTTTATG GAGATGAGGT CTCACTATGT TGTCCAGTCT
16651 GGTCTTGAAT CCTGACCTCA AGTGATCCTC CCCCATCAGC CTCCCAAAGT
16701 GCTGCAATAT TTTAAATCCT GTGGTAGGTC AAGTGGTTGT CTTCTATCTT
16751 GGGGTTTATA AAGTACATGT CAAGAAATTT AGGGTATGGT TAGATTAGCT
16801 TTAAAAATGT CATGTTTTAT AAAAATCAAT GCATCATTTT TCTGATTGAA
16851 AATTTAACAC AAGACTCAGA ATCTTTTTGC AGTAGTGGAA TTACTTTTAT
16901 TATAGATCTT TGCGATAATG AATGATGATA CATCTGGCCA AAAATAGGTA
16951 CTATAGTCTT TTAGGAAAAC AGCTAATCTG CTTGAAATAT GTGTAGAAAT
17001 AATTTAGTGC ATCAGCCCAT ATTGGCAATA ACTTCTCTCT AATTTTTTTT
17051 TATAGAAAAT TTTTACTACT GGAGATGTCA ACAAAGATGG GAAGCTGGAT
17101 TTTGAAGAAT TTATGAAGTA CCTTAAAGAC CATGAGAAGA AAATGAAATT
17151 GGCATTTAAG AGTTTAGACA AAAATAATGA TGGTGTGTCT TTCTTTTGTA
17201 TTTATCACCA GCTATGAAGA AGCATTTATC ATGCTTTCAA GAGTCTAAAA
17251 GGATGCTTAT TTAATCTCTC TGGTTTTAGA TGATAATTAT TATTTGTGTT
17301 AATACTTTTT TTTAGTAATG TGATTTTTAT GTAGAGTTTA TATTATTTAG
17351 TGAAGAAAAC TTATAGATAG CTTTTCTTTT TCATTACTTT GAAATGTAAT
17401 GAATTACATT TCTGAATTAA AAACTGTGGG CAGGGCCTGT TGTAAATGTT
17451 AACTATGGAA CATTATGCTG ATTTGAGTTA AACCTGTAGG TTAAAAATAA
17501 TAATTATATT TTCTTGTCCT CTGGGTAAAA TGAGATTTCT TTTTATTTGT
17551 ATAGAAGAAT GACAGTTGTG TCATCTAAAA TTTAAAAAAC TTTCAGATTA
17601 TCTTGCATCT GTTAGTTTTT TTGGAAGAAT TAATTTAGAG AAGATATCTC
17651 TGATCCTGGA AATTAGGGAA AAATAGCATA TAAACGTTTA AGTGTGTACC
17701 TTCTGGTTAA GATTATGACT TCTATATTTC GATTAATAGG TTGGAGTTTG
17751 TCTTAATCTG TTTTCTGTTG CTGTAATGGA GTACCACAGA CTGGGTAATT
17801 TATGAAGAAA TGAAATTTAT TTCTTATAGT TCTGGAGGCT GGGAAGTTCA
17851 AAGTTGAGCC GAATCTGGTG AGGGCCTCTT ACTATGTCAT AACATGCTAG
17901 CAGGCATCAC AGAGCAAATG CACTACCTCA GATCTCTCTT CCTCTTCTTA
17951 AAAAGCCACT AGTCCCATCA TGGGGGCCCT ACTCTGAAGA CCTTATCTAA
18001 TTCTAATTGG AAATAGGGTC TTGAAGCCCT CATCACTAGA GGTAACCTTT
18051 AACAGGAAGA GAGAATTTAT AAAAATTATA ATGCAGCACC AAATCCCTCC
18101 CTACTTGTGA ATAGTCAAGG TCATTTCATT TACAGACTTG TTATTAAAGA
18151 AACAGGTTAA ACAAATAGAT TGAGAGGAAA TGTGGTTCAT GTCTGAGATC
18201 AGCAAACTTT TTTGTCCAGA AGTCCAGATA ATAAATATTT TAGCTTTGTG
18251 GGTCATGTGG TCTCAGTTGT AGCTACTTGT CTCTGCTGCT GTACCTCAAA
18301 AGCAGCCATG GATAATATGT AAATGAATGG GGATGACTGA TTTCCAATAA
18351 AAACTTTATT TACAAAGATA GTTAATACAC CTTATTTGGC TTGAGGGTTA
18401 TAGTTTGCCA TCCCCTGATT TACAATGAAT ATTAAAGTTT AATTCAAAGC
18451 AAGTTCCTTC AAACAAACAA ACTAAACTCT AGATGATTTT GAAGATTATT
18501 CACATCTGTG ACTCTCAGCC AGGAAGAGCT GAGTTTGGGT TGGAAAGTAG
18551 TACTATTGGA ACATTTGTTG CCCATAAGCC TTACAATATA TGCCCCTAAG
18601 TCTAGCCTTA GTCCAGTCTT CTAGCAAAAC TCAGTTTTCT TTCTTCTCTG
18651 CAAACTTTCA TTCCAACATC GACCCTCTGC AGTTCAGATT GTCTTGCAGG
18701 TCAGATTGTC TGTGTGCTGC TATGGTAGGC AGTAGCTGAG AGATGGAGCT
18751 ACCTTAAGAT CAATTGCCAG ATAATCAGAG GTCAATTATC CCAGTGCATA
18801 AGTAGTGTAC ATATCAATTG TTCATTTTAT AAAATTCTAA ATGAACCAGA
18851 GGCAATAATT AAAGATGAAA TTTTGATGGT ATATTTGTAG GAAATCTACA

FIGURE 3, page 6 of 42

18901 CAATGTTTCC CTAATTTCCC ATGTTTGTGT ATTTTAAAAC AATGTGGCAT
18951 TATTGGTTCA TATTTTTTATT TTTTAGACTT CCTTAATGCA AAACATATAC
19001 AGTTGATCCT CATTATTTGG GGATTCTGTA TTTGCAAATT TGCCTACTCA
19051 ATAAAATTTA TCCCCAAAGT AACCCCAAAA TATATACTCA CAGTACTTTC
19101 CCAGGCATTC ATGGACATGC ACAGAGCAGT GAAAAACTTG AGTTGCTCAG
19151 CATGTACATT CCTAGCTAGT AGAATAAGGC AATACTCTGC CTTCTTGTTT
19201 CAGCTCTCAT ACTATTAACT AGCAAGTATC CCTTTCAAGG TCTATTTTGT
19251 GCCAGTTTTT GCATTTTTGT ATTTTTGTTG GTAATTTCCT TTTTAAAATG
19301 TTCCCCAAAG GTAGTGCTGA AGTGCTGTCT AGTGTTCCTA AGTGCAAGAA
19351 AGCCATAGCA TGCCTTATGG AGAAAATATA TGCGTTGGAT AAGCTTTGCC
19401 CCAAATTCAA TGTTAGTGAA TCAACAGCAC ACATTAAATG AGGTGCCTTC
19451 AAACAGAAAC AGACATAAGA CATGGTTATG TATTAATCAG TTGATGAAAG
19501 TGTTGTAATC AGAGGCTCAC AGGAACCTAA CCCTGTTTTT CCTGTAGGAA
19551 CAATGGTTTG GTATTTGCTA ATTCAGTGTT TGCAATGAAT ATAGAACTTT
19601 ATGGAAGATG ATTGCTGTGA ATAATGAGAA TTAACCATAT CTCTTTAAGA
19651 GTGCATTTCT AAAGGAGAAT ATTCAGAAGG GTATTTGCAT AATTTCTTTA
19701 CTAACAGATG CTGCCTCTCA CTGTCCTTAC ATGGTCCAGA TTCTCATGCT
19751 GCTCCTTCCC TCTCCCCAGG AGGATTCTCT CAGAATCCTG TCATCTCCTC
19801 CAGGGTCCTT TCTCCAAGAA AGTCTATCCT TTCACCACTA ACAGTAATTT
19851 TGGTCTTCCT CTTTTTCTGG AGAAGTCAGC TGTTTATGCT GCTTCAGCAC
19901 CAGACCCTCT CTTACTTTGT TTTGTTTCAT TCTTTTTCAT GTACAGTAGT
19951 CTTAGGATTC TCATGAGCCT GTGAGCTGCT AGAAGGAAAT ACAGCAGTGC
20001 TTACATTTAT TGCTTCTATT TTATTTTCTA TTTTCTCTTC CTGTCTTCTG
20051 ATTGTTCTCC TTCTGTCCAC AAACATGCTC TAATTTCCCT AGTATTAAAA
20101 ATTTTCTGTC TTTTGTTGTT CTTTTATCCT TGCTCCCTTA TTTTTACTGC
20151 CAGATTTTTA TTTTTATTTA TTTATTTTTG AGATGGAGTC TCACTCTGTC
20201 ACCCAGGCTG GGGTGCAGTG GCGCGATCTC AGCTCACTGC AACCTCCGCC
20251 TCCCAGCTTC AAGCAATTTT CCTCTTTTAG CCTCCCAAGT AGCTGGGATT
20301 ATGGGCACCT GCCACCATGC CTGGCTGATT TTTCTATTTT TAGTAGAGAC
20351 GGGGTTTCAC CATGTTGGCC ACACTGCTCT CTAACTGCTG ACCTCAGGTG
20401 AACCACCCGC CTCAGCCTCC AAAAGTGCTG GGATTGCAGG TGTGAGTCAC
20451 TGTGCCTGGC CTTTTACTGC CAGATTTTTA AAAGAATAGT CTGTGCTTTA
20501 GCTCTATTTC CTCATTTACT ACTTCTCTTT AACTCAGTCA TATATGATGT
20551 TTTGCATAGT AAATGTCTAG TAATTTATTA AAAATGTAGA AATAGGTACT
20601 TTTAAAATGA ATAGATCCTA CTTTAATTGA ATTTATCTTG GAGTTAGAAT
20651 ATCTTGATTT GGATTTTAGT TCTGCTACTT CTTAATTACA TTACTTGGTA
20701 AGGCCACTTG TGAAGTCAGT CTCTTTGGAG GAATATTATT TATCTATAAG
20751 GCTGTTACAA TTACTGAATT TTAAAAAATG TGTATTTATT TTTTAATGTA
20801 TTTGTTACAT TTTTAGTATT GATGTTGGGA TAGGCATTTA AGCAAGTCTA
20851 TAACTCACCT ACATGCATAA TTTTGCCTTA ATCAGTTTAA AGCTTTCTCT
20901 TAAATGAGAG ATTTGAAATT CATAATTTCT GTGGTTCTTA TCAGTTCTGA
20951 GTTTTATTTT TTGCCCTTTT TATTTTTTTA AAGGAAAAAT TGAGGCTTCA
21001 GAAATTGTCC AGTCTCTCCA GACACTGGGT CTGACTATTT CTGAACAACA
21051 AGCAGAGTTG ATTCTTCAAA GGTAAGCTCT TCATGTTGGT CAACAATTGA
21101 CTTTCACTTT AATATCCTGC ATTAGAACTC TGTGTTTGTA AGTGTGGCTT
21151 TAAAACACCT CCCTAGTCTT CATTATGTAT ATCCAAGATC TTTTTGTCTT
21201 TTTTCCTCCC ATTCATTTTG TATGTGTACA TTTATCTAAA GTGTAAGAAT
21251 GGGAAGTGTA AGCTCAGACT GGACTCTTTC TTTCAAGGCC TCAAAGGATA
21301 GTGGAATGGC AGGAAGTAAG GTTTTAACTC CATAGATGAG GAGCTGAAGA
21351 GTTTTGGTGT TGCTTTTTCT CCATTTGATT TCTAATGTGA CAGTAAAACT
21401 CATTGATTCA AACTAAGAAG ACTAGCAGAT TCATCACATT ATTTAACCTA
21451 GATGTGACTG GAAAAAAGGG AAATTACTAA GCTCTCCAAG CTAACAAAGA
21501 AATACCTGTT TAAACTTTCA GAAAACAGAA ATGCAAATTT GAACCTTATT
21551 GTCTGGGGCA ATCAGTTTGA CTATTTAAGT CAGACTTTTA TACTCTTAAT
21601 GTTTTGTTTC ATGGGATAGA GCAGTAATCT CTGCAGCCCA GGTGCTCTCA
21651 AATACTCTGT TGCTATAAAC ACAGGGCAGG AACTGATTTT TTATGATAAC
21701 GTAAAACAGA AAAGGACAAT TATATTGTAT TAATATTGTT GTGAATATTT
21751 TCAGTCCTCA CATTGTCTAA AAATCTTTCT AAATGGCTTT GTTATTGAAT
21801 TTATCTCATT TTATATCTGT GCCAACAGCA TTTTCATCCT TTCTCTTCAT
21851 AATTTCTTTT ACAAACAGCT GCTCAAGAGG AAGGCTCAAA GTCTCAAGGC
21901 TGAGCACGTA ATGACTTTTG TTAGTACTAG ATGAGAAGGG CTTTCCTGAG
21951 GAAATGAAAA CCTAAAACAT GAAAAGAAGA TAAACAGAAT TTGGACAGTG
22001 AGATATAGAG CATATAATAT TCTGCTTCTA AAGTAATATT CTTCTAGGAA

22051 AGTGAGGGCG TTTCCCTGGC TGTTAGGCCA GAAATCATAT TCCTATATTT
22101 TCTTTGATAG CTTTAGGAAT AATGCAAATT CTAAGCCCAA GCTTCAGAAT
22151 AGACTAAGAA GTATTAGCTT AGCTGCCATG ACAAAATACC ATAGGCTGGA
22201 TGCATTAAAC AATGGAAATT TAGTTTTTCA CAGGTCTGGG AGCTGGGAAG
22251 TTTAAGATGA GAGTGCCAGC ATGGTTGGGT TGTAGTGAGG GCTCTCTTTC
22301 TGGCTTGCAG ATAGACCCCT TCTCACTGTA TTGTCATATG GCAGAGAGAG
22351 AGAGAGAGAG AGAGAGAGAG AGAGAGAGGG GATCTTTCTC TTGCTTTCTA
22401 TTATAAGGCC ATAGTCCTGT TGGATCAGGG TTCCATTCTT ATGACTTTAT
22451 TTGACTTTAC CCCCCTAAGA TGCTATCTCC AGATATAATC ACACGGTGGG
22501 TTAGGGCCTC AACATTTGGA TTTGGGAGGG ACACAGCTCA GTCCATAGCA
22551 AAGGATAATG CAGAGGGTTG GATATTTAAA AGTAGCTACA CAATTTTTAA
22601 TATAAATATT TTATGGTAAC TTTTTTTTTT TTTTGAGATG GAGTCTAGCT
22651 CTGTTGCCCA GGCTGGAGCG CAATGGTGCG ATCTCAGCTC ACTGCAACCT
22701 CCGCCTCCCA GGTTCAAGCA ATTCTCCTGC CTCAGCCTCC TGAGTAGTTG
22751 GGACTATAGG CACGCGCCAC CACGCCTGGC TATTTTTTTT TTATTTTTAC
22801 TAGAGACGGG TTTGCACCAT ATTGGTCAGG CTTGTCTCGA ACTCCTGACA
22851 TCAGGTGATC CACCCATCTT GGCCTCCCAA AGTGCTGGGA TTACAGAAGT
22901 GAGCCACCGC GCCTAGCCAG CAGCTTTACT GAGATGTAAT TCACATGCCA
22951 TAAATTCACT TTTCTAAAGT ATACAATTCA GTGACTTAAA ACATTTATTT
23001 ATTTTTAAAT TGACAGAATT ACATGTATTT ATCATGTACA ACATGATGTT
23051 TTGAAGTATA TGTACATTGT GGAGTGACTA AGTCTAGCTA ATTAACATGA
23101 TACATCTCAT ACTTAATGAT TTCTGTGGTG AGAACACTTT ACATCCATTC
23151 TCTTAGTATT TTTCAAGAAT ATAATATATT ATTATTAATT GTAGTCTTCA
23201 TGTTGTATAG TGGAGCTCTT GAACTTATTC CTCATGTCAA GCTGAAATTG
23251 TGTGTCCTTT AACACAAACC ATACCCGACT CCCAAAGTAT TCTGCTCTCT
23301 GCTTCTATGA GATTAACTTT TTCTGATTCC ACATGAGTGA GATCATGCAG
23351 TATTTATTTG TCTTTACCTG GCTTATTTCA TTCATATTGT TACAGATAAC
23401 AGGATTTCCT TCTTTTTTTA ATGGCCGAAT AGTTTTCTAT TGTATATGTA
23451 TAGCACATTT TCTCTCTTCA TGCATTGGTG GACACTTAGG TTGATTCCGT
23501 ATCTTGGCTA TCGTGAATAG TGCTATAATG AACATGGGAA TGCACATGGC
23551 TCTTTGACAT ATTGATTTCA TTTTATATAT GTGTATATAT ATATGTATAC
23601 ACACACATAC ATACAGTGGT GGGATTGCAG GATCATATGG TAGTTCTATA
23651 TTTAATTTTT AAAGGAACTC CATACTGCTT TCCATAATGG CTGTATTAGT
23701 TTAACTCCTC ACCAACAGGG TGCAAAAGTT CCCTTTTCTC TACATACTTG
23751 CCAACACTTG TTATCTTTTG TCTCTTTGGT AATAGTCATT CTAAGTGTAG
23801 TATGAGGTGA TATCTCATTG TGGCTTTTAT TTGCATTTCT GTGGTAATTA
23851 GTGATATCGA GCTTTTTTTT TTTTTTGTAC TTTGGCCATT TGTATGTCTT
23901 TGAAAAATGT CTATTGGGGT TTTTTGGTTG TTTATTTGAG GTTTTNNNNN
23951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24251 NNNNNNNCCG GGGTTCCCGT CATTCTCCCT GCCTCAGCCT CCCCGAAGTA
24301 GCTGGGACTA CCAGGGCACC CGCCCACCAC GGCCCGGGCT AATTTTTTGT
24351 ATGTTGAGTA GAGACGGGGT TTCACTGTGT TAGCCAGGAT GGTCTTGATC
24401 TCCTGGCCTC GTGATCTGCC CGCCTCGGCC TCCCAGAGTG CTAGGATTAC
24451 AGGCGTGAGC CACCGCGCCT GGCCTGATTT CTAGTTTTTT ATTATTGTGG
24501 TCGGAAAAGA AACTTGATAT GATTTCATTC TGCTTAAATT TGTTAAGACT
24551 TGTTTTGTGG CCTAACATAT GATATCCCCT GGTGCATGTT CCATGTGCAG
24601 TTGAGAAGAA TGTGTATTCT CTTGCCATTA GGTGAAATGT TTTATGTCTG
24651 ATCTGTCCAT TTGTTCTAGA GTATAGTTTA AGTCTGATGT TTCTTACTGA
24701 TTTTCTGTTG AGATGATTTG TCTATTGCTG AAGGTAGGGT GTTGAAGTCC
24751 CCTACTATTG CTGTATTGCA GTCTCTCTCT CCTTTCAGAC GTATTAATGG
24801 TTTTTATTTT ATTTTATTTG TTGTTGTTGT TGTTGTTGTT GTTGTTTTTG
24851 AGACGGAGTC TCACTCTGTC ACCAGGCTGG AGTGCAGTGG CAGGGTCTCG
24901 GCTCACTGCA GCCCCCGTCT CACGGTTCAA GCGATTCTCC TGCCTCAGCC
24951 TCCCGAGTCG CTGGGACTAC AGGCGCATGC CACCACGCCC AGCTAATTTT
25001 TGTATTTTTA GTAAAGACGG GGTTTCACCA TGTTGGCCAG GATGGTCTTG
25051 ATCTCTTGAC TTCATGATCC ACCCGCCTTG GCCTCCCAAA GTGCTGGGAT
25101 TACAGGTGTG AGCCACCACC CCTGGCCAAT GTTTGGTATT TATCTTTAGG
25151 TGCTCTGATG TTGGGTTCAT ATATATTTAT AAAAAACAAT AGCTACATAA

25201 CTTATTAAGG GATATGCAAT ATAAAATATA TAAATTGTGA CACTGAAAAT
25251 TTAAAATGGG AGGAGTGGAG TAAAAGTACC TTCATATAAC TTACTATTAT
25301 ATCCTCTTAT TGAATTGACC CTTTTATCAT TATATAGGAA CTTTGTTTCT
25351 CCTTTACAAC TTCTGACTTA AAGTTTGTTT TATATGATAT AAGTAAAGTT
25401 ACTCCTGCTC TCCTTTGGTT TCTGTTTCCA TGGAATATCT TTTTCCATTC
25451 CTTCACCATC AGTCTGTGTG TATTTTTACA GATGAAATGA GTCTGTCATG
25501 GGCAGCATAT AGTTGGATCT AGTTTTTTTA ATCCACTCAG ACACTGTGTT
25551 TTTTGATTGG ATAATTTAAT CCATTCATGT TCAAGGTAAT TATTGATAAG
25601 TAAGGACTTT GTACTACCAT TTTGCTTATT GTTTCATGGT TCTTTTATAG
25651 ATCCTTTATT CTTTTCTTCC TCTCTTGCTG TCTTTTTTTT GTGGTTAAGT
25701 GATTTTCTCT AGTGGTATGT TTTGATTTCT TGCTTTTTAT TTTTTGTGTA
25751 TCTCCTATTG GTTTTTGGTT TGTGGTTACC AAGAGGTTAC AAAAAACATC
25801 TTAAGAGTTA TAATAGTTTA TTTTAACTTG ATAACTTAAT TTTTATTGCA
25851 AAAACCCCCC AAAACAAAAA AATCTACACT TTTACTTAAT CCCCTGAAAT
25901 TTTGAATTTT TGATGTCACA GTTTACCTCT TTTCATATTG TGTATCCCTT
25951 AAATTATTGT AGCTATTATT ACTTTTAATA GTTTTCTCTT TCCTACTACA
26001 GATGTAAGTG ATTTGCATAC CATCATTACA GTATTATTTT GAATTTACCT
26051 GTGTACTTTT TTTTATCAGC CAGTTTTATA CTTTCAGATG TTTTTGTGTT
26101 ACTCATTAGC ATCTTTTTCT TTCAGCTTGA GGAGCTCCTT TTACGTTTCT
26151 TATAAAATAG GTGCGGTCAT GATTATCTCC CTCAGCTATT GTTTGTCTGG
26201 GAAAGTATCT CTCCTTCATT TCTGAAGGAC ACTTTGCTGG GTACATTACC
26251 CTTGGTTGGT ATTTTTCTCC TTGAACGCTT TAAATATATC ATCCCTTTCT
26301 CTCCTGACCT GTTAGGTCTC TGCTGACCAG TCTGTTTCCA ACCATATTGG
26351 GACTGTCTTA TATGTTATTT GCTTCTTATC TTTTGCTGTT TTCAGGATCC
26401 TCTCATTGTC TTTGATTTTT GATAGTTTGA TTGTAATATG TCTTGGGGTA
26451 GTCTTGTTTG GATTGAATCT GATTAGAGAC CTTGGACTTT TCCTGCATGT
26501 AGATATTTAC CTCTTTCTCC AGGTTTGGAA AATTTTCTGT TACTGTTTCT
26551 TTAATTAAGC TTTTTACCCC TTTTATCTTC CTTTTCTCCT TCTTCAACTC
26601 CTGTGACTCA AAACTTTGCT CTTTTGATGC TGTTCCATAA ATCTTGTAAG
26651 CTTTCTTCAT TCATTTTCAT TCTTTTTTCT CCTCTGTGTA TTTTCAAATA
26701 ACCTGTCTTT GAGTTCATAG TTTCTTTCTT CTTCTTGATC ACTTCTGCAG
26751 TTGATGCTCC CATATTGCAT TTTAATTTTG TTCATTGTAT TTTTCAGCCC
26801 CATGATTTCT GTTTGATTTT TTCTTTTATT ATTTCATCTC TTTATTACCT
26851 TTCTCTTTGT GGTCACTCGT TATTTTCCTA ATTTCATTGA ATTGTTTCTT
26901 TGTATTTTCT TGAAGTTTGC TGAGCTTTCT TTGAATTCTA TGTCAGTTCA
26951 TACATCTCTG TTTCTTTAGG GATGGTCGCT GGTACTTTAT TTTGTTTCTT
27001 TAGTGGTGTC ATTTGTTCCT GATTGTTGTT GATGTTTGTG GCCTTGTGTT
27051 TACATCTGTG CATTTGAAGA AGTAGGCACT TATTTCAGTC TTTGCAGACT
27101 GGCTTTGTCT GAGAATGCCC TTCAACAGTC AGCCTGTCTA GAGATTCTTT
27151 AATATTTAAT TAAATATCTT TAATATTTTG AAGAACTTCC AAATTGTTTC
27201 TAAAGTGGCT GCACCATTTT ATAATCCCAG CAGCAATGAA TGAAGGTTTC
27251 AGTTTCTCCA TAGCTATATG AATACTCATT ACTGTCTGTC TTTTCATTTT
27301 TTGATTTTTA TTTTTTTTTT GAGAAAGGGT CTTGCTCTGT CATCCCATCT
27351 GGAGTGCAAT GGCACAATCA TGGCTCATTG CAGCCTCAAC TTCCCTGGCT
27401 CAATTGATCC TCTCACCTCC TGAGTACCTG GGACTACAGG CATTGTACCA
27451 CAATGCCTGG CTAATTTTTA TATTTTTTGT AGAGATGTGG TTTTGCCATG
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27551 ACTGGGTAAT TTATAAAGGA AAGAGGTTTA ATTGACTCAC TTTTGCTTGG
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27701 AAAAACCCTT ATAAAATAAT CAGATCTCAT GAGAAGTTAC TCACTATCAT
27751 GAGAACATCA GAATGAGGGT AGCCTCCTCC ATGATTCAAT TACCTCCCAC
27801 TGGGTCCCTC ACGTGACATG TGGGGATTAT TGGAACTATA ATTCAAAATG
27851 AGATTTGGGT GAGGACACAG CCAAACCATA TCATTTTTGC CCTGGTCCCT
27901 CCCAAATCCC ATGTTCTCAC ATTGCAAAAC ACAATAATGC CTTTCCAGCA
27951 GTCCCCCAGC GTCTTAACTC ATTCCAGCGT TAACCTAAAA GTCCAAGGTT
28001 TCATCAGAGA CAAGGCAAGT CCCTTCTGCC TATAAGCCTG TAAAATCAAA
28051 AGCAAGGTAG TTATTATACT TCCTAGATAC AATGAGGGTA CAGGCATTGA
28101 TTAAATATAC TTGTTCCAAA TGGGAGAAAT TGGCCAAAAT GAAGGGGCTA
28151 CAGGCCCCAA GTAAGTCCGA AATCTAGTGG AATAGTCAAA TCTTAAAGCT
28201 CCAAAATGAT CTCCTTTGAC TCCACATCAC ACATCCAGCT CATGCTAATG
28251 CAAGAAGTGG GCTCCCATGG CCTTGGGCAT CTGCACTCCT GTGGCTTTTC
28301 AGGGTACAGA CCCCCTTCTG GCTCTTTTCA CAGGCTGGCG TTGAGTGTCT

28351 GTGGCTTTTC CAGGTGCATG GTGCAAGCTG TCGGTGGATC TACTATTCTG
28401 GGTACTGGAG GATGGTGGCC CTCTTTTCAC AGCTCCACTA GGCAGTGCTC
28451 CAGTGGGGAC TCTGTGTGAA GGCTCCAACC CCACATTTCC CTTCTGCACT
28501 GCCCTAGCGG AGGTTCTCCT CAAGGGCTCC ACCCCTGCAG CAAACTTCTG
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28601 CTCAAACCTT AATTCTTATC TTCTGTGTAC CCGCAGACTC AACACCTTGT
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28701 TGTACCTTGG CTCCTTTTAG CCATGGCTGG GATGCAGGGC ACCAAGTCCT
28751 GAGACTGCAC AAAGCAGCAA GGCCCTGGGC CTGGCCCAGG AAACCATTTT
28801 TTCCTCCTGG GCCTCTGGGC CTATGATGGG AGGGCCCTTC CTGAAGACCT
28851 CTGAAGTGCC CTGGAGGCAT TTTCCCCATT GTCTTAGTGA TTAACATTTC
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29001 AACTTTTGTC CTCTGCTTCC TGTGGAATGC TTTGCCACTT AGAAATTTCT
29051 TCTGCCTGAT ACCCCAAATC ATCTCTCTTA GGTTCAAAGT TCCACAGATC
29101 TCTAGGGCAG GGGCAAAAAG CCACCAGTCT CTTTGCTATA GCATAACAAG
29151 AGTCATCTTT GCTCCAGTTC CCAACAAGTT CCTCATCTCC ATCTGAGATC
29201 ATCTCAGCCT GGACTTCATT GCCCATATTA CTGTCAGCAT TTTGGTCAAA
29251 GCAATTCAAC AAGTCTCTGG GAACTTACAA ACTTTCCCAC CTCTTTTTGT
29301 CTTCTGAGCT CTCCAAATTT TTAAGAAGTT CCAAACTTTC CCAGTCTTCT
29351 TCTGAACCTT CCTAACTGTT CCAACCTCTG CCTGTTACCC AGTTCCAAAG
29401 TCAGTTCCAT ATTTTTGGGT ATCCTTATAG TAGCACCCAA CTCCTAGTAC
29451 CAATTTACTG TATTAGTTCA TTCTCACGCT GCTATAAAGA ACCACCTGAG
29501 AATGGGTATT TTATAAAGGA AAGAGGTTTA ATTGACTCAC AGTTTCGCGT
29551 GGCTGGGGAG GCCTCAGATA ACTTACAGCC ATAGCAGAAA GGGAAGCAAA
29601 CATGTCCTTC ACATGGTGGC AGGAAGAAGA AGTGCTGAGC AAAGAGGGAA
29651 AAGCCCTATA AAACCATCAT ATCTCGTGAG AACTCACTCA CTATCATGAG
29701 AACAGCAGCA TGGGGTTGAC CACCCCCCAT AATTCAATTA CCTCCCACCA
29751 GCTGTCTCCC GTGACACATG GAAATTATGG GAACTACAAC TCAAGATGAG
29801 ATTTGGGTGG GGACACAGCC AAACCATATC ATCTAGGCTG GTATCGAAAT
29851 CCTGGGCTCA AGCAATCCAC CCACCTTGCC CTACCAAAGT GCTGGGATTA
29901 CAGGCATGAG CCACCATATC TGAACTGTCT TTTGATTTCT TTTGATTTTA
29951 ACCATCCATT GTTTCTGCTT CTCTAGATAA CCCTGACTAA TATATAATTG
30001 GTATGAAGTG ATATCTCATG GCTTTGATTT ATATTTCTTT CATGGCTAGT
30051 GACTTTTTTT GTACTTTTGG GATATTGTTA TTATTATTAT TATTATTACT
30101 AGTGTTTATA CTTCTTCAGT AAAAGTGTTA GAAACAATTT TTAAAGGCAG
30151 AATGTGACCA GAGTTTCCTG TAGTTATATA ACCATCATGG ACCTTCCCTC
30201 AAGTGCTAAG CCATTAGTGT TACTCATGTC ACTCCAAATG TCAGCTTGTT
30251 TTCTTCCATT TCACTGTCTC TTTGTGTCCC AAACTTGAAT TCATGGGAAA
30301 AACATCTGAA TGGTGCTTAA TATGGTTTGG ATATTTGTCC CCTCCAAATC
30351 TCATGTTGAA ATATGACCTC CAGTGTTGGA AGTAGGGACT ACTTGGGTCA
30401 CGAGAGTGGA TCCTTCATTA ATGGCTTGGT AATAAGTGAA CTCTATTAGT
30451 TCATGAAAGC TGGTTGTTGA TAAGAGCCTG GCATCTCATT TCTCTTGTCC
30501 TTCTCTCACC ATCTGACACA CTTGCTCACC TTTTTCTTC AGCCATGAGT
30551 AAAAGCTTCC TGAGGTCTCA CCAGAAACTG AGCAGATGTT GGTGCCATGC
30601 TTGTACAGTC TGTAGAACTG TGAGCCAAAT AAGCCTCTTT TCTTTATAAA
30651 TTACCGAGTC TCAGGTGTTC GTTTAAAACA ACACAAAACA GACTAACACA
30701 GTGTTGATTG AAACAGCTGT GACTGGGTCA TCAGGGTGTA AGAGAGGAGT
30751 CACTGAGTTG AAATATAGCC TCCTACTTAC ACCTGTTCAG TAGAAGCTGT
30801 AGATATGAAG TAGCTGAAGC AGGCATTCCC TCTGAAACAT GTGTTTCACA
30851 TATGTCATAA TTATCTTCTG CTCTCATTTT TCTTTTAGGC TTTTGTCTCC
30901 ATCTCATTTC CCCTGTTTAC TCTCATTTTC ATATCTTTAC ATTTCTTTCT
30951 CCAGAATTGT TCAGAAGCTT GGAACCCTTC ACTCCAGTTA TTCTTTGACT
31001 ATGCAATTTG TTTCTGTGCT TCATGGCACT TATGGTTTGT AATCCTTGAC
31051 TTGTTTGTAT AGCTCAGTGG TTAGGAGTAC AGTTTGGAGT TAGAATGCCT
31101 GGGTTGAAAC TCTTAATTCT ACTCTACTTA CTAGTCTTGT GACTATAACA
31151 AAATTCTTAG CCTCTCTTTG TCTGTAAAAT GGAGAGTATA GTAAATACAT
31201 GGGCTTGTTT TAAGGATTAA ATGAGTTAAC ATGTGAAATA CTTAGAACAA
31251 TGCCTGGCAA ATGCTCAATG AATATTGAGT ATTGCTTGCT TTTGTTTAGT
31301 GCCATGCCTG TTGTTCCCAC TGAGGGCACA GACCATGTGT ATCTGGTTAA
31351 CAGTTCTATG TCCACCACGT TGCAATAATG GACTCTCAGA AAATATTGAA
31401 GAATATGTTA AAGAATGAGT AGAATTATGC TACTGAAAAG GGTGAGTGGA
31451 AGGTAGGTAG GGGAAAGGAC ATATACAGCC CTGGAGGCAG CATATATGGG

FIGURE 3, page 10 of 42

31501 GAATGGGTCA CACAGTGTTT CTTGGTACTC TCTAGACCAT AGTGGGCCAC
31551 CTCTTAGCTA GTGGCCTATG GATTATTTCA GCAGTCTGTT GGAAACATCC
31601 ATGAATATGA TAATAATGAC CCATTTGTGG GTTCTAAGAA AAAGGACAAC
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31701 TGTATTAAAC TGTTCTAAAA TTCTTACCTT ATTTAGGATG ATGGGGTCAG
31751 ACATTAACTT TAGACTTTGT TATATATATG TGGTAAAATT TCAAGGTAAA
31801 CCATTGAAAC TGTAGTAGTT GAGTATATAA CTTCCAAATC AGGGGGGAAA
31851 GAAATGGAAT AAGAAAATAA ATACATAAAC ATAAGATTGA AACAATCCAA
31901 TGAAGAGTAG AGAGAAGAGG GAAAAACATA GAAAGAATGA GATAATTAGA
31951 AAGCAATAGG TAAGATGTGA GAAATAAATT CAAGTACAGT AAAACTCCAC
32001 TAAAATGTGC CCTGCAGTAA TGTTGGGGCA TGATTTCCCT TCATCCCCAT
32051 TCTCAAATGG GGCAGCCTAA ATAGCGTTCT TATCCTGTTT CCCTGGGGGT
32101 TTGAGGTGGG TGACGAGTAA GTTAGAAGAT AATCACCTTC TGATCAGTTA
32151 GGACTTTCTC AGTTTAGTCT TCAATTAATA AAAATTAATG TAAATTTCAT
32201 CAGAAGGCAG AGATTGTCAG ATGAAAGAAC AAGCAAAATA AAAGTCTTAC
32251 TGAAAAAAAG CTGGGGTAGC TATGTTAATA TCAACTGTTA ATTATTATTA
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32401 TTGATAAAAT TCTGGGGATT AATTGGCAAA TCCATCATAG TGGTGAGAGA
32451 TTTTAACACA ATTCTTCCTG TATTTGATAG GTCAAGCAGA GAAAAACTTT
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32601 ATGGAACATG TATAAAAATT GATTTCGTAG TAGGCCATAA AGCCAGGTTC
32651 AACACATTTC AAAGAACTGG TATCACAAGA ACTGCTTTCT CTGACCACTA
32701 TGCATTAAAA TAGAAGTTAA TTACAGACAT AAATTATAAA AATGCCAATA
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33201 AATTTCTAGA AAAATATAAC TTACTGGGAC TGAATGAAGA AGCAACAGCT
33251 TATAGTACCT AAGCAATTGA AGAGATTGGG TCAGTAATTT AAAATTTTCT
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45751 GTGTGTAATG AACTTTTAAT CTTTGGCATT CTATGACTAT TCAAACATTT
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45901 AGACTCTTAG AGCAGCAATG TAATTTTGAA AATTATTCTA AAGCTGAGGT
45951 TAGCAGAAAA AGATCTGGCT TTATAGACTG ACTTTGCTAT TTACTAGCAG
46001 TGTAGCATTG GGCTGGCCAG AGTGGAAAGA GGGAATGGAA AAGAATTAAT
46051 ATGTATTTGC TCACTGTGGT AACCCAGTTA ATCCTTGCAG CAGCCCAGTG
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46151 GACTTTTCCT TTACAACAAA TGAGAGGGGG AATGCAGTAT CTTTGCCTCC
46201 AGTGCTCCTG GTTCTCATGC TGCATGAAAC CTCTGAGGTC TCATTTTCCT
46251 TCATTCTGGG ATGGGGATAA GAATATCTAA TAAGAATGGT TTAAGAATCA
46301 AGCAATATCA GGTATGTGAT AATGTCTGGT ACACTGGAAT AACCTATTGG
46351 AACATAGTAG TTGTTTACAA AATATTTTTA AAACTTTGTT ATACTTATGG
46401 TCAACACTTT TTATATTTGT CTGTAGATTT CTGTACAAAA AGATTCTGAC
46451 ACTGTTTTAA GCCAGCATTC CTTCAGAATG TACCCAAATC TCAAAATTTA
46501 TTTAGGGGCA AAGCTAATGC TTTAAAGAAA AAGGAGAGGG GATTGGTGTG
46551 TGTTTTTCTT TAGGAACAGT AGTAACTTGA CTTTTAGAGA ACTTGAATAA
46601 GCATTTATTT TTTCCTTTGT CCTATTTTAT TGTGAAGTTT ATTTATTTAA
46651 AATAAAATGG ATTTCTCTGG AATTTAGTTT CTGCAAATTT GAGGAGTTTC
46701 CAAAGTCAAC CTTCAGGTTT GATACTTCTC TAGAAAGACT CACATAACTC
46751 ACTGAAAGCT TATTACCCCT GGTTATGGTT TATTACGGGG AAAAGATGCG
46801 GATGAAAATC AGTCAAGTAA AGAAGCACAT AGGGCAGAGC TTCTGTTGTC
46851 CTCTCCCTGT GGAGTCTCCA TGTCTTACTT TCCTGGCACT GTTATGTGGC
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46951 GGTGTGCAGA GTTCTTATTG GGGCCTGTTT TCATACTGGC CACATGGCTG
47001 GCCTTCAGAA TTCAACCCGT TCTGTGAGTG TGTGTGTGTG TGTGTGTGTG
47051 TGTGTGTGTG TGTTTAGTGG TAGTCACCCC TTTTATGTGA GCTGAAACAA
47101 TCAGAAGAAT AGCTGATTTG TTTAATTATT TTTGGTGTAT TGGACTTAAT
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47201 CACATCTGTA GTATAAGCCA AGTAATTTAT CAGTACTCAC AGGATGGGTA
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47251 CATGTTGTAA TGAATTTATT GCCTAGAGAG GGCCTCAAAA TATGCCAAAG
47301 AGGGTGCAAT TTTTATTTTT GGTTTCAGGC TGTATGCATT CCAGTGTTGG
47351 TAGCCCTGAT ATACACAATA TCCAAACCAT TTCAGACCCA TTTACAGTTC
47401 ATGTCTGTAC TACTTCTTGA GGAGAGGGAG TAACATATTA CTTTAAATTA
47451 TATGTAATAA TATACATACA TTAAATTATA TGTAATAATA TAATATTATT
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48301 TTCATTCTGA ATCCTGAGCA GAAGCAGCAC ACTAACATAA GTTTTATGAA
48351 AGTGTCACAA TCTAACCTCT GGAAGGAAAA CTATAAGTTG AAGTCCTTTG
48401 TGTAATTTGA CGTTGCTGTA AAATTGAGCT GAGTTTGGAG TGACACCTCC
48451 ATGAAGGCAG GGGCGTGGCT TCTTCCCCAT GTACTCCAGC ACCTAGACAG
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48601 GGATTATTTG AGCTATTGCT TCAGCCTAAC TCAATGTAAA GGGGAAATAC
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50651 AATAAATAAA GGGGAAGATA AGGATTGGAA ACAGAAGGAG CAGCATGTGG
50701 ACAGAAATGT AGGCACAAGA AGGCATCACT CACTGAAGAG ACTGAAAGTG
50751 GTTCACTGTG CCTCAAGACT GGTGGAGTGT GTTTCCGGAA AGATAATGAT
50801 GAAAGAGCTG GACAGATAAA CAGGGGCCAA ATGTAATAGG AGTCTGGATT
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51101 CTCACTGACT GACTGGATAT GGAGGTGAGA AAGAGAAGAG TCAAGAATGA
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51201 GGTTCCATTT TGTGCATGCT GAGTTTGAGA TGTGTGGGAC ATGTACAGGG
51251 AGCTGTCCAG TAAGCAATTG GGTATATCAG CTAGCCATTA AGAGAGAGAT
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51351 ACTCAAGAAG AGCTTATAAA TGAGAAGAAT TCTAGGAATA AGTCCAAAGG
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51601 TCTGTGAAGT AATGAAATGA GAAACCATGC TGAAATGAGC TTAAAGTGAA
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51851 AGTAAAGTGG TGCAATCTCA TCTCACTGCA ACCTCTGCCT CCTAGGTTCA
51901 AGTGATTCTT CTGCCTCAAC CTCCTGAGTA GTTNNNNNNN NNNNNNNNNN
51951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
52001 NNNNNNNNNN NNNNNNNNNN NNNNNTGCCT CAGCCTCCCG AAATGCTGGG
52051 ATTGCAGGAG TGAGCCCCCC GTGCCTGGCC TGGAGGGAGG ATTTTGATTT
52101 GACTTTAATG TGCCTGTTGC TGAAGGAAGC ATGTCAATAC AAATAAAGAA
52151 GTTGAAAACA TAGGTAAGAG AGGTTGATTA ACCCGGTAGG TGTTTCAAGG
52201 GAGTTTGTGT GTAGGGAAAG GGAGTGGGAG ATGGAAAGGG GCTGGGGGAG
52251 ACAGGTTCTA TCCAGAGACT GTTAAAAGGA TTAGTCTTTG ATTACAAGAA
52301 GAACTCTTCT TATACGTGTT TGGGAAGAAA AAATATGTGA GTAGCTATGG
52351 ATAATTTTGC AGGAGGTGGG CAGAATACCA AGATATTCTG CCTGGTGGCC
52401 TCTCTACTCT TCCTTGAGCT CCTGAGAAAG GATGTGATCT GAGAATGAGG
52451 GAGGAAGTGG TATTGGAAGC TGGAGGAGAA TGGAGAAGAT CAAAATGGTT
52501 AGTCTAACAA ATGGGAGAGA ACTGAGATAG ACAAAAGGAT TTCAGGGTGG
52551 TTTTGAGGGC TCAGTTAAGT CTCCTTTAGG AAGGTTCAGT TCTGTAGCCT
52601 TGGCAAGTTA CTTAAAGTCT CTGTGACTAT TACCTCATCT CTAAGATGGG
52651 GACTAAGCTT GGTGACATAG TTTTACATAC CAGGCACAGT GCCTGACTTT
52701 TTGGCTCTGT CCTGAAGTCT TCCCTTTGTA TATGGTATGT TTCGGGGAAT
52751 AGGAGCCTCA AGCACTTATC CTTTAAATAT TTATCCTCCA TCAGTCACTA
52801 AACGTTTACT CTGTACTTTT GATAGGTGCT GTGGGGGTCC AGGGTATAAA
52851 AGGTACCTTC AAAGTTACTG TTAAAGTGCA GGAAGGTTTT TAAGCAAATT
52901 ATGTTTAATG ATTTTGACAA TCTGACATGC AGGAAAATTA ATAGGGCCTA
52951 TGCAGAAGAG GAGTTTTATG TAACACTCTG TAGTTCAGGA AACAGAGCCC
53001 TTGGAAGCAG TGATCTCTCT GGGGAGGAAT GTCTGGTATT TGGGAATCTC
53051 ATGAAATGAT AATATACTTA ATTTTTATCA TGAGCAGCAA AACACAGATT
53101 TGCTAGGAGA AAGTCATCGT ATGTTGTTGC ATTGGGCACT TTAGATCCCA
53151 GGGAACAGAA ACTGGCTGGC ACAGGAATGG GCATCACTGT GGGGATGGAT
53201 CATGTAGGGG AAGGATCCCT GGAGAAGTCC AGGAGGTGAG ACTTCCCCCT
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53301 CCTCTGGTGA CAGCAGCTGC TTACCTCTGG AGACCCCCTC ACATTTCTGA
53351 GAGAAGGAAT CTGGCTTGCC TGGCTAATTC CCATGGTCTA TGTTTGGGCA
53401 GAATGTCTTA GCAAGTTGTG TAAAGATAGT GTATTCATAT ATTAATAATA
53451 ATAATAACAT CTACTGAACA TTTGCTAGGT GTTCAGACCT GCACTAACCG
53501 TGTTACAAGT ATTATTTTTT TGTAATCCTT TCCATAACCC TGTGAGGTAA

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53551 GTACTGTTAT CACAGACAAG GAAACCACAA TGTGGACCTG TTCATGAACT
53601 TGCTCGAGGC CACGTGGCTC TGGAGTTCCA GCTCAGGTCT GCCTGACTCT
53651 CAATCCCATG ATATTAATAT ACTGGCCAGT CACTATTTTG GCTGTATTGG
53701 GGTCATATTT ATACCCTTGG TCCAGTTAGC TATGTTGGGT CACTTTAGTA
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53851 ACCTATTTAT TCATTTTATT TGCACTGGTG AAAATAAACT CATCTTTTAA
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54301 CAAGCCAGTT TGATTTCTAG TGAGCGTTCT CTTCTCAGCT TGTAGACAGC
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54601 TTGTTTATAC AGTACAAGAA GTTACTTACT GAAGAAGGAC AAAAAATAGG
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54901 CACAGTCAAG ATGGTAGTCA GAGCTTGGAA TCAGCTGGAG GCGGATTCCA
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55001 AGTTCCTTAT CACGTGAGCC TTTCTGTAGG CTGCCTGAGT ATCCTCAAAA
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55201 GGTGTTAATA ACCGGAGACA AATATCACTG GGGGTCACTT TAGAGGCTGG
55251 CTGCCACTTT AGAGGCTGGC TGCCATTCCT GTCCAAAGAG TTTCTGTACC
55301 ATAAATTTAA TAATGGAATC TCAGGATTTG ATTATATGGT GATTATCCTA
55351 ATTAGACATC CTTTCATTAG TGCATAGGTT GGCAAAACAC AGACCTACGG
55401 ACTGTTTCAT ACAGCCCTTG ACCTAAGAAT GCCTTTTACA TTTTTAAAAA
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55501 TCACAATTAA AAGAACTAGA GAAGCAAGAG CAAACAAATT CAAAAGATAG
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55701 GAGAATCAAA TAGCCCCAAT AAAAAATGAT AAAGGGGATA TCACCACCAA
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55801 CAAATAAACT AGAAAATCTA GAAGAAATGG ATAAATTCCT GGACACATAC
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55901 AACATGTTCT GAAATTGAGG CAGTAATTAA TAGCCTACCA ACCAAAAAAA
55951 ACCCAGGACC AGACAGATTC ATAGCCGAAT TCTACCAGAG GTACAAAGAG
56001 GAGCTGATGC CATTCCTTCT GAAATTATTC AAACAATAGA AAAAGAGAGA
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58551 ACAATTTTTA AAAAGTAGGC AAAAACAAAA GAAAAGAAAA GTAATATACA
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58651 TCTTTACAGG AAAAGTTTTC CAACTACTGC TTTATAGCAA AAATAATATT
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58801 ACAGCTTTTT TTAAGCATCT TAATATGATT GTTTATATTA CTCCACACAC
58851 CTCTCAAAAA AACTTAATAC CCTATTTTTC CTCTCATATC CTCCCATATC
58901 AGTTAATAGT ATCACCTTCC CAACTCCCCA CTGCCCCATC CTGTGTTCCA
58951 AGCTAGAAGT ATTGGGGTTA TCCTTTATAC TACCATTTCC CTCACCTTCC
59001 AGATGCAGGT GGTCACCAGT CAGTTTTGTT AAGACATCAA TAGATTATCT
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59201 GGTATTTGTT CCATGTAAAA TTACTTCATT TGAATCCCAT GATGATAGAG
59251 TTAATATGAA CAATCATATT TTGTTTTTTT TTATATCCAG GTTATGAAAA
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59451 TGTATGAGGT GAGTTTGTAG AAATCTTTTG AATTGGAAAA TGCAGTTAGA
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59951 TGTGCCTTGA AGAAACTGAA GGTCTGGTGG GGGAGACAAA CGACTAAAAC
60001 TCAGCGTGGT TATCTGTGCT GCGACAGACA TGAGCCAGGG TGCATGTTAG
60051 GATGAGACCT AAGCTACAGC GTAGAGGAAG AGTGGAATGT GTAATGAAAA
60101 GAAGAGTCGA ATTTTTTTTT TAAAGAGCTT TATTGAGATT TAGTTCATAT
60151 TCCTTACATT TCACTCATTT GAAGTGTACA AGCAAATGGT TTTTGGCTTC
60201 TTACATAATT TTTAAAAATT ATTATAAAAT ATAAAATTTG CCATTTTACT
60251 AATTTTAAGT GTACAATTCA GTGGCATTAA TTACATTCAC AATATTGTGC
60301 AACCATCAAC ACTATTTCCA AATCCTTTTC CTCACTCCAA ACAGAAACAC
60351 CTTAACCTTT AAGCAATAAC TTCCTACCCT CCGTAACTCA AACCTTTGGT
60401 AACCTCTAAT CTGCTTTCTA TGTCTAGGAA TTTACCCATT CAAGATATCT
60451 TATAAGTAGA ATCATACAGT ATTTTTCTTT TTGTGTCTGA TTTATTACTC
60501 TTAGCATAAT GTCTCTAAGG TTTGTTCATG TTGTAGCATG TATCAGAACT
60551 TCATTTCTTT TCATGGCTGA GTAATATTCC GTTATGTGTA TATACCACAT
60601 TTTGTTTAGT CCTTCATCTG TTGAAGAGCA TTTGGATTAT TTCTACTTTT
60651 CCAACATTGT GAATAATGCT GCAGTGAACA TTGGCATCTG CGTATCTGTT
60701 CGAGTCTATG CCTTCAATTC CTTTGGGTAT ATATCTCAGA ATGGAATTGC
60751 TGAGCCATAT GGTCATTCTG TGTTTAGCTT TTAGGAACTA TGAGACTGTT
60801 TTCCATAGTG GCTGCACTTA CATTCTCACC AGCAACATAC AAAGGTTCCA
60851 GTTTTTCCAC GTCCTTATTA ACACTTAATT TCCATTTTAA AAAAGCTTAT
60901 TTTTATTATG GCCGTCCTCT TAGGTGTGAG GTGGTATGGT TCAGGACTTT
60951 ACTTCTTGTG CTGAGTTTTT TAAAAAATTG TGATTAAAAA CACATAACAT
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61051 CTGTTTGTGG TTTGTTGTGC AACAGATCTC TAGAACTTTT TCACTTCTCA
61101 AAACTTAAAC TCTATAGTCA TTAAACAACA GCTCCCAATT TCCCCTTCAC
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61251 TATTTCATGT AACATAGTTT CCTCATGATT CATCCATATG ATAGCATACA
61301 ACAGGACTTT TTTGTTTTTA AGGCTGAATA ATAATTTGTT GGGTATATAT
61351 ATCACATTTT CTTTATTCAT CTGTTGATGG ACATTTGGAT TGTTTCTACA
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61451 CTTCAAGATA CTGTTTTCAG TTCTTTTTGA CATATACTCA GAAGTGGAAT
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61601 GTACACCAAG ATTCCAATTT CTCCATGTCC TCCCCAACAC CATTAAGTGG
61651 GGTGGTGGTC TACTACTATT GCTGTGTTGC TGTTTATTCC TCCCTTCAGT
61701 TCTGTAAGTG TTTGCTTCAT ATATTTAGGA GCTTAATATT AGGTCCATAT
61751 GAAGTTATAA TTTCTTCCTG GTAAAGTGAC CCATTTATCA TTATGTAATG
61801 TCCATCTTTG TCTCTTGTGA CAGTTTGTGT CTTAAAATCT ATTTTGTCTG
61851 ATGTAATTAT GGCCACCCCT TTTCTCTTTG GGTTCCCGTT TTTATGGAAT
61901 ATCTTTTTCC ATCCTTTCAC TTTCAGCTTA TGTGTGTCCT TAGATCTAAA
61951 GTGAGTCTCA TAGATAAGGT ATAGTTGATT CTGTATGTGT TATTCACTCA
62001 GCAATTTATA TCTTTTAGTT AGGGGATTTA ATCCATTTAC ATTTAAAGCA
62051 GTTACTGATA GGGAAGGACT TACTGTTGTC ATTTGGCTAG CTACCTTTTT
62101 ATCTTTGTCC TGTGGCTTTT CTGTTTTTCC CTTCCTCTCT TCCTGGCTTC
62151 TTCTGTGTTT TGTTGATTTT TTTTTTTTTT GTAGTGATAT GTTCTGATTC
62201 CCTTCTCATT TCCCTTTGTG TGCATTCTAT AGATGCTATT TTTGTGGTTA
62251 CCATTGCAAC TACATAAAGC ATACTAAAGT TATAGCAACT TATTTTAAGC
62301 TGTTTACAAC TTAACTTCAG TGGTATATAA AACTCTATTT CTTTACATAT
62351 TTCACCTCCT CCCCACAAAC TTTATGTCTT TTGATATTGT ATATCCTTAA
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63001 ATGAAATACA GGGACCTAGA GTAACAGGGA TAAAGTATGG CCTTTTGATC
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63101 TGGCTCATGC CTATAATCTC AGCACTTTGG GAGGCCGAGG CGGGCGGATC
63151 ACCTGAGGTC AGGAGTTTGA GATCAGCCTT GCCAGCATGG TGAAACCCTG
63201 TCTCTACTAA CAGTACAAAG ATTAGCTGGG CGTGGTGGTG GGTGCCTGTA
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63451 AATATATGTA ACGTGTAAAA TGAGATACAA TTAGTAGAAT TATATTATTT
63501 TATTAATACT CACCATAAGA GGTGTTCTTT AGATCCTGCA GCGTTTGCTG
63551 CGCAGTTCAC GTTTGTTTAG AAGAATGTCA GTAACCGGTG CAAACCTCAT
63601 GTGTTCCGCA CCCCCAGTGG CCTCCCACCT CTCCACAGAG TCACCGCCTC
63651 CTGCAGTGCC TGCTGCTTCT GCAAATGCGT GGCCTCATCC TGCAGAAACG
63701 GGGCTTCTCA TGAGGTTGAG AATAGCTGTG AAAATGTTTA CGTTGAAGTT
63751 GTAGAGTTCG TTAATTATTT TCTTCTTTAT TTCTCTGGCA GCTCTTGAAG
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64401 AGTGTTGCGT AGACCCTACA AGTTTTGAGC TGTGATTCCT CCTCACTGTG
64451 ACACTGTCTC CATTGTTGGC TTTGATTACA CTGTACCATC CTGGTTGTTC
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64951 AAAGATGAGT GGGAGTTAGC TGGGCACAGG CCAGTGGAGT GGGAACAGAA
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65451 GTTAGTGGGA ATTTCAAAGC CTTTAATAAT CTAGCCCCAC TTTGTTCACT
65501 CTCTGTGTAA TAACCACATA CAACAATTGG CTGCATCTCC ATAGCACATG
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65801 AGCCCTACCA TTTTCTACTT AGATTTTTTT AGGACAAATT TCTCCATCTT
65851 TCTAAGCCTC CAATTGCTCA CTTACAAAAT TGATATAACA TTTACCTTGC
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65951 TAAATAACTA TTATTACCAT CATTACTATA GTTAGGACAC TCACTGTTAG
66001 GTGCTATACA AAGAGGATCA TAAAAGGGAT GTTGTCTTGG GCTTCTTGGA
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66101 TGTTTGTTGT CATAATAATG AAACATACTT GAATATTAAA TTACCCTCTT

66151 TTTTTATTTT TTAGCCATGT TAGAAGGTTC CCCACAGCTG AATATGGTTG
66201 GCCTCTTTCG ACGAATTATT TCCAAAGAAG GAATACCAGG ACTTTACAGA
66251 GGCATCACCC CAAACTTCAT GAAGGTGCTC CCTGCTGTAG GCATCAGTTA
66301 TGTGGTTTAT GAAAATATGA AGCAAACTTT AGGAGTAACC CAGAAATGAT
66351 GTTGCATTTT TTGCTTTAGC CTGATAATTG AAACTTTCAA CAATCTCTGG
66401 AGTGACTTTT TCTCCTCGAA TTGAAACAAG TCTATGGCAA AAGAAGCTGC
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67151 GTTTCCTACC TTTTGAATCA GATTCCGTTT TAGTCAGGAA GACTTCTTGG
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67701 GAACCTACCT CTTTTATTTT CTGAACCAAA GAGAAAGATG GACTGGTGTT
67751 TGTGAAACAT TTTTAAAAAT GTAGTTTCAT TTATATTAGT TATGTTTGAT
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67901 GATCAGCTCT TTCTATTTTT ACTCGTAAAA ATTATGGAAA TGAATAATTT
67951 TGCTAACAAC TTTGAAATTT CAAACTTCTG GAAAATATGA AAATATTCAT
68001 TGTTCATTAT GAATTTAAAT TGTAAGGTAT GAATGTGATT TGTCTGTACA
68051 TCTTGTATCT TTTCCAAAAA ATGATTCTGT ATCTTTTGGA AAAAAGCCGA
68101 GAGTTGAAGA TAGTATATTT CTGGTAGTAC TGAATATTTA CTTACAGTTT
68151 CTATCAAAAA TATATATTTG TTTCTAAAAT TACTTGTTTT CCAGTTTTTA
68201 TTTTTTTTAG AGAAAATTCT TAAGTCTCAG TTTCCTAATT GAAAAAAAAA
68251 AATTATAAAT AAAGCAAAAA TTGTATCCTA CAGCTTAGCT AGCTTAGATG
68301 TTTGGCACCA GTTTGAATCA TGCTTTTTAC AGCTGGCTCC ATGTAGTCTT
68351 TCCAAACATT TTGGCCTTTC CTGAGCAGCC CTTGTAGATA TTGTCTGTAT
68401 GATGCATTTT GACACAAGGT GATATTTTTT GTGATATCAA AATTCCACAT
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68651 CATAAGACTG CAGAGAAATT CTGCATTTCA ACTCCAATAC TATCCAGACT
68701 TCAGAAATAA CTTATCAGTT ATTTCTGTAA GCTTCTTGCT TACCTGGATA
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69001 GTTGCATTTG TAAAAATGTG GCATGGCTTC CTCATCCCCC AATAGGAACT
69051 TTGCCAGCCC TTTTGTTCTC ATGGAACTTC CTTTTTTGAA AAGAGCACCA
69101 AAGGAGTAAA AATACTGTGG AGGGAGCAAC CCTCCTTTGC CATATGCTCT
69151 CATTGGGAGA CATGTGGAGC AGTCTGAAGT CATTTAGGCC ACTCTCTGGG
69201 AGAGCACATC CTATGATGTT CTCCCAGCCT AGCCCCTTCC ACTGTGCTCA
69251 AGTCCAAGCT GACCAGCTTT CTGACCACAG TGTAAACAAA GATGATTGTC

69301 AGTGGGCCCC AGAATCCTAT ACCCAGA

FEATURES:

Start:	2132
Exon:	2132-2314
Intron:	2315-17055
Exon:	17056-17182
Intron:	17183-20983
Exon:	20984-21071
Intron:	21072-41719
Exon:	41720-41831
Intron:	41832-45391
Exon:	45392-45550
Intron:	45551-47878
Exon:	47879-48031
Intron:	48032-54612
Exon:	54613-54720
Intron:	54721-59290
Exon:	59291-59458
Intron:	59459-63791
Exon:	63792-63942
Intron:	63943-66164
Exon:	66165-66346
Stop:	66347

CHROMOSOME MAP POSITION:

Chromosome 1

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
1722	G	C A	Beyond ORF(5')
1767	C	G A	Beyond ORF(5')
1840	C	G	Beyond ORF(5')
1857	T	G	Beyond ORF(5')
1945	G	T	Beyond ORF(5')
2007	A	C	Beyond ORF(5')
2769	C	G	Intron
3664	C	T	Intron
3827	G	A	Intron
4113	C	T	Intron
4337	A	G	Intron
4473	G	A	Intron
6455	T	G	Intron
6533	T	G A	Intron
6919	G	C	Intron
7305	G	A	Intron
7340	A	G	Intron
7466	A	G	Intron
7589	G	C	Intron
7810	A	C	Intron
9104	G	A	Intron
9503	A	T	Intron
9898	G	C	Intron
10196	T	C	Intron
12327	C	G A	Intron
13749	G	A	Intron
14150	T	C	Intron
14529	G	A	Intron
14653	G	A	Intron
15871	A	G	Intron
19244	G	A	Intron

19387	T	G	Intron
19447	C	G	Intron
20076	T	C	Intron
20492	T	-	Intron
20868	T	C	Intron
20941	T	C	Intron
21116	C	T	Intron
21701	G	A	Intron
21710	A	-	Intron
21826	C	T	Intron
21840	-	T	Intron
21841	-	C T	Intron
21843	-	C	Intron
22045	C	A T	Intron
22061	G	T	Intron
22348	-	A G	Intron
22682	A	G T	Intron
22783	-	T	Intron
23448	A	G	Intron
24960	G	A	Intron
24983	T	C	Intron
25390	T	C	Intron
26060	C	T	Intron
30245	C	G	Intron
33664	G	T	Intron
33883	C	A	Intron
34373	G	A	Intron
34558	G	T	Intron
43929	T	A	Intron
44309	T	- C	Intron
44997	T	G	Intron
46538	A	G	Intron
48153	T	C	Intron
48288	G	T	Intron
48412	G	A	Intron
48446	C	G	Intron
48456	G	C	Intron
48789	C	-	Intron
48859	G	C	Intron
49126	A	G	Intron
49378	T	G	Intron
49482	A	C	Intron
49741	G	A	Intron
49840	A	G	Intron
50102	G	A	Intron
50109	C	G T	Intron
50747	G	A	Intron
51272	G	A	Intron
52842	G	A	Intron
61837	A	G	Intron
62018	A	G	Intron
65562	A	G	Intron
65780	G	A	Intron
66092	G	A	Intron
66617	C	T	Beyond ORF(3')
66892	G	A	Beyond ORF(3')
67263	G	A	Beyond ORF(3')
67651	G	T	Beyond ORF(3')
67935	C	T	Beyond ORF(3')
69000	T	G	Beyond ORF(3')
69134	C	T	Beyond ORF(3')

Context:

DNA Position	
1722	TTGCCCACGCAGATGGCTGTTGATCTTTTCTGCAACAAATCCAGGAGTTTCTCCTTTTTG TTTTATAATTGCTCCAATAGATGCTTTAGGATTTAACTCTCTGCTTTTTAAAGCAGAATC GCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCAT GGCCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCGAG AGGGTCTTTAAGTGGAGTAACCAGTCTTCAAGACCCCGCTCCCAAGCCACCGACGCGCTG [G,C,A] CGCTGCAGCCCTGGACCTGCTGGGGGCCTCTTCCTCGGACCCGCATGCTGACAGCGGGAC TGGCAACTGGGCAGAGGTCGACCCCGGGTCCGCACAGCACCTCCCGAGACCCAGCTCCCA GCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGGCCAGTGCCGCCGAGGCCAGCGCGG CGAGCTCCTCCCCAGCAGCGGCGGGACGGCCACACCCTGCGCGCCGCGCGGGCTCGGGTG GGGTCTCCGCTCCTGCGCCCTGCGCGCCGCAGCCGCACCCCCGACGGCGCCCCAAACGCT
1767	AGTTTCTCCTTTTTGTTTTATAATTGCTCCAATAGATGCTTTAGGATTTAACTCTCTGCT TTTTAAAGCAGAATCGCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGA GACAATGCCCTCCATGGCCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCA AGGCTCCGGCCCGAGAGGGTCTTTAAGTGGAGTAACCAGTCTTCAAGACCCCGCTCCCAA GCCACCGACGCGCTGACGCTGCAGCCCTGGACCTGCTGGGGGCCTCTTCCTCGGACCCGC [C,G,A] TGCTGACAGCGGGACTGGCAACTGGGCAGAGGTCGACCCCGGGTCCGCACAGCACCTCCC GAGACCCAGCTCCCAGCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGGCCAGTGCCG CCGAGGCCAGCGCGGCGAGCTCCTCCCCAGCAGCGGCGGGACGGCCACACCCTGCGCGCC GCGCGGGCTCGGGTGGGGTCTCCGCTCCTGCGCCCTGCGCGCCGCAGCCGCACCCCCGAC GGCGCCCCAAACGCTGTTGCGCCGCGCGCCCCGCCCAGCCCGGCCTCGCGCTGGTCCCGG
1840	TCGCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCC ATGGCCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCG AGAGGGTCTTTAAGTGGAGTAACCAGTCTTCAAGACCCCGCTCCCAAGCCACCGACGCGC TGACGCTGCAGCCCTGGACCTGCTGGGGGCCTCTTCCTCGGACCCGCATGCTGACAGCGG GACTGGCAACTGGGCAGAGGTCGACCCCGGGTCCGCACAGCACCTCCCGAGACCCAGCTC [C,G] CAGCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGGCCAGTGCCGCCGAGGCCAGCGC GGCGAGCTCCTCCCCAGCAGCGGCGGGACGGCCACACCCTGCGCGCCGCGCGGGCTCGGG TGGGGTCTCCGCTCCTGCGCCCTGCGCGCCGCAGCCGCACCCCCGACGGCGCCCCAAACG CTGTTGCGCCGCGCGCCCCGCCCAGCCCGGCCTCGCGCTGGTCCCGGTCTCGCCCCGCAG CCCTCGATCTCCCGTGACTTCCTCGGCCAGGCCGCCTGCGCCTCTGGGACCATGTTGCGC
1857	CAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCATGGCCCAGTTTCCAGG CAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCGAGAGGGTCTTTAAGTGG AGTAACCAGTCTTCAAGACCCCGCTCCCAAGCCACCGACGCGCTGACGCTGCAGCCCTGG ACCTGCTGGGGGCCTCTTCCTCGGACCCGCATGCTGACAGCGGGACTGGCAACTGGGCAG AGGTCGACCCCGGGTCCGCACAGCACCTCCCGAGACCCAGCTCCCAGCTCCCTCACTTCC [T,G] GCTCTCTGGAGGCGGGCCCGGCCAGTGCCGCCGAGGCCAGCGCGGCGAGCTCCTCCCCAG CAGCGGCGGGACGGCCACACCCTGCGCGCCGCGCGGGCTCGGGTGGGGTCTCCGCTCCTG CGCCCTGCGCGCCGCAGCCGCACCCCCGACGGCGCCCCAAACGCTGTTGCGCCGCGCGCC CCGCCCAGCCCGGCCTCGCGCTGGTCCCGGTCTCGCCCCGCAGCCCTCGATCTCCCGTGA CTTCCTCGGCCAGGCCGCCTGCGCCTCTGGGACCATGTTGCGCTGGCTGCGGGACTTCGT
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[G,T]
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CAAGTGAAACATAATAGAGAGCCCAGAAACAGACCCATCCATATTTTGGATTTGTCACGT
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33883 TAAAGAAGACTCAGTATAGAAAAGATGTACCTTCTCTCCAAATTGGTGATAGAGATTCAA
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[C,A]
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34373 TATCTTTATCTCAGTGTAGGGAAGAATTTATTTTAAAAAGAAGACACAAAAGGCCATACA
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CAAGAGCATCTGTACTTGGACAGCATAGAGTGGAAAGACAAAGAGAAGGTATTTGCCAGC
TTTATAACTTGAAGGATTAGAATGAATGATATAAAGAACTATGTAAATAAGAAAAAGACAT
ACAACCGGTTAGAAAAACGGGCAAAGACATGAACAGCATATTTCACGTGAAGGAAACAGC

FIGURE 3, page 35 of 42

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          [G,A]
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34558     ACTTGAAGGATTAGAATGAATGATATAAAGAACTATGTAAATAAGAAAAAGACATACAAC
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          TTAAGCTACAGAGTTTGTAATTCATTTATTTATTCAATAAATACTCAGTGGCAGGCACTG
          [G,T]
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          TGCTTATGTGTGGGGAGTTGGGTGGTGGGGTCAAACAACAATTACATTAAAATAGAAAAT
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          GACTAGGACTCTCATGCAGATATACCTCTGTGCTGGGACAAATGAAAGTTTAAGTGTAAT
          TTCCCATATGCAAGTCAAAATAAAAAGTGACACTAGAAAACACAATAATGAATATCTGAA

43929     GGCATTTAAGTATTCTGCCATAGGGAAGTGTAAAAGTTGTAGGCTTTTACTTTTTATAGG
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          ATCTTTTTGCTTCATCTGCTTAGCATTTCATACCAGTTTGTTTTCCACCAAACTTTCAAA
          TTTTGATTGTTTCATTAATATTCTGCATACTGATGTAAACCAAGTTCTATTATTGTGCAA
          [T,A]
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          TGGTGCGATCTCGGCTCTCTGCAAACTCGGCCTCCGGGGTTCACGCCATTCTCCTGCCTC
          AGCCACCGGAGTAGCTGGGACTACAGGCACCCACCACTGCGCCTGGCTAATTTTTTTTGT
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44309     TTGAGACGGAGTCTTGCTCTGTTGCCCAGGCTAGAGTGCAGTGGTGCGATCTCGGCTCTC
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          ACTACAGGCACCCACCACTGCGCCTGGCTAATTTTTTTTGTATTTTTAGTAGAGACGGGG
          TTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTTGTAATCCGCCCGCCTCGCC
          TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCCGGCCTTTTTTTTTTTTTTTT
          [T,-,C]
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          CAGGAGTTCACATTGCCACTAGTAACAATGCCTAAGCTTACATAAAGCATTATAAAATTG
          TTGGTGATTAGTGCCTTCTCAGCTATGAGTATAAGATAATATTATACTAGTAGTTCAGTT
          GCCTAGATAAATTGTACACTATGTGAAGTTTTATTTACATAATTCTTACGGTATTTTTTA
          AGGTAGTTGATAACAGTTGAGACTACAATTGTATCTCCATTTTATTGATAGTAAAATGAA

44997     GAATTGTAAAAATATTATTATAGAATTGTTTCTCTCAAACTATAGTAATGTAGAATAGGT
          TGAAGGGGTGATGATTTGAAACAATACCTCTCCATTAGCTAAATTTTATATAGAATCTAT
          TGCATGTTTTAAATGATAAGTCAGATTTATAAAAATATTTTTATAAACAGTAGGAAATGA
          GTTTAGGGGTATTCACATACAGTTTTAATTTTTATTTACATATTTAAAACATATCATGGT
          ATAAATATGATGTGGATATAAATTTGAGATAAAGGAAGTATTGTTTAAGAATTGATGAAC
          [T,G]
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          ATACTGTGAATCTATGATGAATGAAAGAAAGTTGTAACTGTTGGTTTTGTATATTTGTAA
          TTACTGTTTATTTTCATTTCTTGTGAACTGATACTGTACTTTGTTCATTGTGAGTAGACA
          ACTTATAATCTATGTACTCAAATTGGTTTAGTATAAATTCTAGGGAATGAAGTTCATATT

46538     TGTTATACTTATGGTCAACACTTTTTATATTTGTCTGTAGATTTCTGTACAAAAAGATTC
          TGACACTGTTTTAAGCCAGCATTCCTTCAGAATGTACCCAAATCTCAAAATTTATTTAGG
          GGCAAAGCTAATGCTTTAAAGAAAAAGGAGA
          [A,G]
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          AAGCATTTATTTTTTCCTTTGTCCTATTTTATTGTGAAGTTTATTTATTTAAAATAAAAT
          GGATTTCTCTGGAATTTAGTTTCTGCAAATTTGAGGAGTTTCCAAAGTCAACCTTCAGGT
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[T,C]
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48288 AAATTGCTCCTGAGACAGCTGTTAAATTCTGGGCATATGAACAGGTAATTGTTATCACCC
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[G,T]
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48446 CATATACCCCATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTC
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[C,G]
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48456 ATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACCAA
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[G,C]
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48789 GCACCTAGACAGAGCTTGGCATGTGATAAGTTTCAAGCGAGTGTTGAATGAGTCAATGAA

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[C,-]
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[G,C]
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[A,G]
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[T,G]
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49482 TCCATGGGTATTGCAAGCAAATATGCACATTTTGCTTTATGCCATTTGTCAGATTCTTAC
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CTTTATAGTATTGTGATTTCTGCACACTAACTTTCTTAGACATGAAGAGAAAGCTGTCTA
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GCTGAAGGTCCATTCATCCCTCGGGGCTCTCTAAAAGCCACCTTCCTGTGACAAGCATAT
[A,C]
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[G,A]
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50109 ATAGTAGTGTCATTGTATCATTGACAGTGTAATAGTGTGGGGTAGTGTTCTTGTGGTTTC
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[C,G,T]
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50747 CCAGCCTGGGCAACGTGGCAAAACCCCATTTCTACAAAAAATATAAAAATTAGTTGGACG
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[G,A]
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61837 GAGGAACCTCCATGTCATTTTCCATAGTAACTAGACCTTTTTGTTTTTTAACATTTCTAT
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[A,G]
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[A,G]
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[A,G]
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[C,T]

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